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(54) Title: METHYLATION ALTERED DNA SEQUENCES AS MARKERS ASSOCIATED WITH HUMAN CANCER

(57) Abstract: There is disclosed (103) novel methylation-altered DNA sequences ("marker sequences") that have distinct methylation patterns in cancer, compared to normal tissue. In many instances, these marker sequences represent novel sequences not found in the GenBank data base, and none of these marker sequences have previously been characterized with respect to their methylation pattern in human cancers including, but not limited to those of bladder and prostate. These (103) sequences have utility as diagnosis, prognostic and therapeutic markers in the treatment of human cancer, and as reagents in kits for detecting methylated CpG-containing nucleic acids.

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METHYLATION ALTERED DNA SEQUENCES AS MARKERS ASSOCIATED WITH HUMAN CANCER

5   **Cross-Reference to Related Applications**

This application claims priority to U.S. Patent Application Serial No. 09/699,243, filed October 27, 2000.

Technical Field of the Invention

10   The present invention relates to novel human DNA sequences that exhibit altered methylation patterns (hypermethylation or hypomethylation) in cancer patients. These novel methylation-altered DNA sequences are useful as diagnostic, prognostic and therapeutic markers for human cancer.

15   **Background of the Invention**

The identification of early genetic changes in tumorigenesis is a primary focus in molecular cancer research. Characterization of the nature and pattern of cancer-associated genetic alterations will allow for early detection, diagnosis and treatment of cancer. Such genetic alterations in vertebrates fall generally into one of three categories: gain or loss of

20   genetic material; mutation of genetic material; or methylation at cytosine residues in CpG dinucleotides within "CpG islands." Among these, DNA methylation is uniquely reversible, and changes in methylation state are known to affect gene expression (*e.g.*, transcriptional initiation of genes where CpG islands located at or near the promoter region) or genomic stability.

25   *Methylation of CpG dinucleotides within CpG islands.* DNA, in higher order eukaryotic organisms, is methylated only at cytosine residues located 5' to guanosine residues in CpG dinucleotides. This covalent modification of the C-5 position of the cytosine base by the enzyme DNA (cytosine-5)-methyltransferase results in the formation of 5-methylcytosine (5-mCyt), and gives this base unique properties (*e.g.*, susceptibility to

30   undergo spontaneous deamination). This enzymatic conversion is the only epigenetic modification of DNA known to exist in vertebrates, and is essential for normal embryonic development (Bird, A.P., *Cell* 70:5-8, 1992; Laird & Jaenisch, *Human Molecular Genetics* 3:1487-1495, 1994; Li et al., *Cell* 69:915-926, 1992).

The presence of 5-mCyt at CpG dinucleotides has resulted in the 5-fold depletion of

35   this sequence in the genome during the course of vertebrate evolution (Schroderet & Gartler, *Proc. Nat. Acad. Sci. USA* 89:957-961, 1992), presumably due to spontaneous deamination of 5-mCyt to Thymidine. Certain areas of the genome, however, do not show such depletion,

and are referred to as "CpG islands" (Bird, A.P., *Nature* 321:209-213, 1986; Gardiner-Garden & Frommer, *J. Mol. Biol.* 196:261-282, 1987). These CpG islands comprise only approximately 1% of the vertebrate genome, yet account for about 15% of the total number of genomic CpG dinucleotides (Antequera & Bird, *Proc. Nat. Acad. Sci. USA* 90:11995-11999,

5   1993). CpG islands contain the expected (*i.e.*, the non-evolutionarily depleted) frequency of CpGs (with an Observed/Expected Ratio[1] >0.6), are GC-rich (with a GC Content[2] >0.5) and are typically between about 0.2 to about 1 kb in length.

     Methylation within CpG islands affects gene expression. CpG islands are located upstream of many housekeeping and tissue-specific genes, but may also extend into gene
10   coding regions (Cross & Bird, *Current Opinions in Genetics and Development* 5:309-314, 1995; Larsen et al., *Genomics* 13:1095-1107, 1992). The methylation of cytosines within CpG islands in somatic tissues is believed to affect gene expression. Methylation has been inversely correlated with gene activity and may lead to decreased gene expression by a variety of mechanisms including inhibition of transcription initiation (Bird, A.P., *Nature*
15   321:209-213, 1986; Delgado et al., *EMBO Journal* 17:2426-2435, 1998), disruption of local chromatin structure (Counts & Goodman, *Molecular Carcinogenesis* 11:185-188, 1994; Antequera et al., *Cell* 62:503-514, 1990), and recruitment of proteins that interact specifically with methylated sequences and thereby directly or indirectly prevent transcription factor binding (Bird, A.P., *Cell* 70:5-8, 1992; Counts & Goodman, *Molecular Carcinogenesis*
20   11:185-188, 1994; Cedar, H., *Cell* 53:3-4, 1988). Many studies have demonstrated the effect of methylation of CpG islands on gene expression (e.g., the *CDKN2A/p16* gene; Gonzalez-Zulueta et al., *Cancer Research* 55:4531-4535, 1995), but most CpG islands on autosomal genes remain unmethylated in the germline, and methylation of these islands is usually independent of gene expression. Tissue-specific genes are typically unmethylated in the
25   respective target organs but are methylated in the germline and in non-expressing adult tissues, while CpG islands of constitutively expressed housekeeping genes are normally unmethylated in the germline and in somatic tissues.

     Methylation within CpG islands affects the expression of genes involved in cancer. Data from a group of studies show the presence of altered methylation in cancer cells relative
30   to non-cancerous cells. These studies show not only alteration of the overall genomic levels of DNA methylation, but also changes in the distribution of methyl groups. For example, abnormal methylation of CpG islands that are associated with tumor suppressor genes or oncogenes within a cell may cause altered gene expression. Such altered gene expression may provide a population of cells with a selective growth advantage and thereby result in
35   selection of these cells to the detriment of the organism (*i.e.*, cancer).

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[1] Calculated as: [number of CpG sites / (number of C bases X number of G bases)] X band length for each fragment.

[2] Calculated as: (number of C bases + number of G bases) / band length for each fragment.

Insufficient correlative data. Unfortunately, the mere knowledge of the basic existence of altered methylation of CpG dinucleotides within CpG islands of cancer cells relative to normal cells, or of the fact that in particular instances such methylation changes result in altered gene expression (or chromatin structure or stability), is inadequate to allow

5   for effective diagnostic, prognostic and therapeutic application of this knowledge. This is because only a limited number of CpG islands have been characterized, and thus there is insufficient knowledge, as to which particular CpG islands, among many, are actually involved in, or show significant correlation with cancer or the etiology thereof. Moreover, complex methylation patterns, involving a plurality of methylation-altered DNA sequences,

10   including those that may have the sequence composition to qualify as CpG islands, may exist in particular cancers.

Therefore there is a need in the art to identify and characterize specific methylation altered DNA sequences, and to correlate them with cancer to allow for their diagnostic, prognostic and therapeutic application.

15

Summary of the Invention

The present invention provides for a diagnostic or prognostic assay for cancer, comprising: obtaining a tissue sample from a test tissue; performing a methylation assay on DNA derived from the tissue sample, wherein the methylation assay determines the

20   methylation state of a CpG dinucleotide within a DNA sequence of the DNA, and wherein the DNA sequence is a sequence selected from the group consisting of sequences of SEQ ID NOS:1-103, sequences having a nucleotide sequence at least 90% identical to sequences of SEQ ID NOS:1-103, CpG island sequences associated with sequences of SEQ ID NOS:1-103, CpG island sequences associated with sequences having a nucleotide sequence at least

25   90% identical to sequences of SEQ ID NOS:1-103, and combinations thereof, wherein the CpG island sequence associated with the sequence of the particular SEQ ID NO is that contiguous sequence of genomic DNA that encompasses at least one nucleotide of the particular SEQ ID NO sequence, and satisfies the criteria of having both a frequency of CpG dinucleotides corresponding to an Observed/Expected Ratio >0.6, and a GC Content >0.5;

30   and determining a diagnosis or prognosis based, at least in part, upon the methylation state of the CpG dinucleotide within the DNA sequence. Preferably, the DNA sequence is a sequence selected from the group consisting of CpG island sequences associated with sequences of SEQ ID NOS:1-103, CpG island sequences associated with sequences having a nucleotide sequence at least 90% identical to sequences of SEQ ID NOS:1-103, and

35   combinations thereof. Preferably, the DNA sequence is a sequence selected from the group consisting of CpG island sequences associated with sequences of SEQ ID NOS: 2, 4, 6, 7, 9-16, 19, 20, 22-33, 35-43, 48, 51-55, 59, 60, 64, 71, 76, 78-81, 84 and 87-90, and combinations thereof. Preferably, the methylation assay procedure is selected from the group

consisting of MethyLight, MS-SnuPE (methylation-sensitive single nucleotide primer
extension), MSP (methylation-specific PCR), MCA (methylated CpG island amplification),
COBRA (combined bisulfite restriction analysis), and combinations thereof. Preferably, the
methylation state of the CpG dinucleotide within the DNA sequence is that of
hypermethylation, hypomethylation or normal methylation. Preferably, the cancer is selected
from the group consisting of bladder cancer, prostate cancer, colon cancer, lung cancer, renal
cancer, leukemia, breast cancer, uterine cancer, astrocytoma, glioblastoma, and
neuroblastoma. Preferably, the cancer is bladder cancer, or prostate cancer.

The present invention further provides a kit useful for the detection of a methylated
CpG-containing nucleic acid comprising a carrier means containing one or more containers
comprising: a container containing a probe or primer which hybridizes to any region of a
sequence selected from the group consisting of SEQ ID NOS:1-103, and sequences having a
nucleotide sequence at least 90% identical to sequences of SEQ ID NOS:1-103; and
additional standard methylation assay reagents required to affect detection of methylated
CpG-containing nucleic acid based on the probe or primer. Preferably, the additional
standard methylation assay reagents are standard reagents for performing a methylation assay
from the group consisting of MethyLight, MS-SNuPE, MSP, MCA, COBRA, and
combinations thereof. Preferably, the probe or primer comprises at least about 12 to 15
nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-103, and
sequences having a nucleotide sequence at least 90% identical to sequences of SEQ ID
NOS:1-103.

The present invention further provides an isolated nucleic acid molecule comprising a
methylated or unmethylated polynucleotide sequence selected from the group consisting of
SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:12, SEQ ID
NO:13, SEQ ID NO:18, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:32, SEQ ID NO:34,
SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:68, SEQ ID NO:69,
SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:82, SEQ ID
NO:83, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:97,
and SEQ ID NO:100. Preferably the nucleic acid is methylated. Preferably, the nucleic acid
is unmethylated.

Detailed Description of the Invention
Definitions:

"GC Content" refers, within a particular DNA sequence, to the [(number of C bases
+ number of G bases) / band length for each fragment].

"Observed/Expected Ratio" ("O/E Ratio") refers to the frequency of CpG

dinucleotides within a particular DNA sequence, and corresponds to the [number of CpG sites / (number of C bases X number of G bases)] X band length for each fragment.

"CpG Island" refers to a contiguous region of genomic DNA that satisfies the criteria of (1) having a frequency of CpG dinucleotides corresponding to an "Observed/Expected Ratio" >0.6), and (2) having a "GC Content" >0.5. CpG islands are typically, but not always, between about 0.2 to about 1 kb in length. A CpG island sequence associated with a particular SEQ ID NO sequence of the present invention is that contiguous sequence of genomic DNA that encompasses at least one nucleotide of the particular SEQ ID NO sequence, and satisfies the criteria of having both a frequency of CpG dinucleotides corresponding to an Observed/Expected Ratio >0.6), and a GC Content >0.5.

"Methylation state" refers to the presence or absence of 5-methylcytosine ("5-mCyt") at one or a plurality of CpG dinucleotides within a DNA sequence.

"Hypermethylation" refers to the methylation state corresponding to an *increased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

"Hypomethylation" refers to the methylation state corresponding to a *decreased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

"Methylation assay" refers to any assay for determining the methylation state of a CpG dinucleotide within a sequence of DNA.

"MS.AP-PCR" (Methylation-Sensitive Arbitrarily-Primed Polymerase Chain Reaction) refers to the art-recognized technology that allows for a global scan of the genome using CG-rich primers to focus on the regions most likely to contain CpG dinucleotides, and described by Gonzalgo et al., *Cancer Research* 57:594-599, 1997.

"MethyLight" refers to the art-recognized fluorescence-based real-time PCR technique described by Eads et al., *Cancer Res.* 59:2302-2306, 1999.

"Ms-SNuPE" (Methylation-sensitive Single Nucleotide Primer Extension) refers to the art-recognized assay described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

"MSP" (Methylation-specific PCR) refers to the art-recognized methylation assay described by Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996, and by US Patent No. 5,786,146.

"COBRA" (Combined Bisulfite Restriction Analysis) refers to the art-recognized methylation assay described by Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997.

"MCA" (Methylated CpG Island Amplification) refers to the methylation assay described by Toyota et al., *Cancer Res.* 59:2307-12, 1999, and in WO 00/26401A1.

Overview

The present invention provides for 103 DNA sequences (*i.e.*, "marker sequences")
having distinct methylation patterns in cancer, as compared to normal tissue. These
5   methylation-altered DNA sequence embodiments correspond to 103 DNA fragments isolated
from bladder and prostate cancer patients, and in many instances, represent novel sequences
not found in the GenBank database. *None* of the instant sequence embodiments have
previously been characterized with respect to their methylation pattern in human cancers
including, but not limited to, those of the bladder and prostate. The significance of such
10   methylation patterns lies in the value of altered fragments as potential prognostic, diagnostic
and therapeutic markers in the treatment of human cancers.

Identification of Methylation-altered Marker Sequences in Genomic DNA

The MS.AP-PCR technique was used to scan the genomes of bladder or prostate
15   cancer patients for DNA methylation changes relative to normal individuals, because the
pattern is known to be highly conserved. A total of 103 DNA sequence embodiments
(methylation-altered DNA sequences; "marker sequences") were isolated and characterized
as having distinct methylation patterns in cancer, as compared to normal tissue.

Methods for the Identification of Marker Sequences in Genomic DNA. There are a
20   variety of art-recognized genome scanning methods that have been used to identify altered
methylation sites in cancer cells. For example, one method involves restriction landmark
genomic scanning (Kawai et al., *Mol. Cell. Biol.* 14:7421-7427, 1994), another involves
MCA (methylated CpG island amplification; Toyota et al., *Cancer Res.* 59:2307-12, 1999),
and yet another involves MS.AP-PCR (Methylation-Sensitive Arbitrarily-Primed Polymerase
25   Chain Reaction; Gonzalgo et al., *Cancer Res.* 57:594-599, 1997), which allows for a global
scan of the genome using CG-rich primers to focus on the regions most likely to contain CpG
dinucleotides. The MS.AP-PCR technique used in the present invention is a rapid and
efficient method to screen ("scan") for altered methylation patterns in genomic DNA and to
isolate specific sequences associated with these changes.
30   Briefly, genomic DNA from the tissue of bladder or prostate cancer patients was
prepared using standard, art-recognized methods. Restriction enzymes (*e.g.*, HpaII) with
different sensitivities to cytosine methylation in their recognition sites were used to digest
these genomic DNAs prior to arbitrarily primed PCR amplification with GC-rich primers.
Fragments that showed differential methylation (*e.g.*, *hypermethylation* or *hypomethylation*,
35   based on the methylation sensitivity of the restriction enzyme, or upon DNA sequence
analysis or Ms-SNuPE analysis; Gonzalgo & Jones, *Nucleic Acids Res* 25:2529-2531, 1997)
were cloned and sequenced after resolving the PCR products on high-resolution
polyacrylamide gels. The cloned fragments were used as probes for Southern blot analysis to

confirm differential methylation of these regions in the tissue. Methods for DNA cloning, sequencing, PCR, high-resolution polyacrylamide gel resolution and Southern blot analysis are well known by those of ordinary skill in the relevant art.

    Results. A total of 500 DNA fragments that underwent either hypermethylation (an
5   increase in the level of methylation relative to normal) or hypomethylation (a decrease in the level of methylation relative to normal) were isolated from the scanned patients genomic DNA. A total of 178 of these fragments were sequenced, of which 103 were *novel* in that they corresponded to DNA loci whose methylation pattern had not previously been characterized. The corresponding sequences are disclosed as [SEQ ID NOS:1-103], wherein
10 for certain sequences, the letter "n" refers to an undetermined nucleotide base.

    Novel marker sequences identified by MS.AP-PCR. Table I shows an *overall* summary of methylation patterns and sequence data corresponding to the 103 DNA fragments identified by MS.AP-PCR. A total of 103 fragments were sequenced following identification as becoming either hypermethylated (gain of methylation; noted as having a
15 hypermethylation pattern) or hypomethylated (loss of methylation; noted as having a hypomethylation pattern) relative to normal tissue. For the fragments of each category, the "Average GC Content" is shown, calculated as (number of C bases + number of G bases)/band length for each fragment, as well as the average Observed/Expected Ratio ("O/E Ratio"), calculated as [number of CpG sites/(number of C bases X number of G bases)] X
20 band length for each fragment. Additionally, the percent of fragments that qualify as CpG islands is listed, and corresponds to the percentage of all fragments within each category that have sequence compositions that satisfy the criteria of having a "GC Content" >0.5 and an "O/E Ratio" >0.6.

    Thus, of these 103 fragments identified by MS.AP-PCR, 60 showed hypermethylation
25 (Table I, upper row; Table II, [SEQ ID NOS:1-60]) while 43 showed hypomethylation (Table I, lower row; Table II, [SEQ ID NOS:61-103]). Moreover, 55 (43 hypermethylated, and 12 hypomethylated) of the 103 fragments correspond to CpG islands (*i.e.*, fulfill the criteria of a GC content >0.5 and an Observed/Expected Ratio >0.6;), whereas the other 48 (17 hypermethylated and 31 hypomethylated) fragments do not meet the criteria for CpG islands
30 (*see* Table II).

TABLE I. Summary of 103 DNA Fragments Identified by MS.AP-PCR

DNA Fragment Type	Methylation Pattern (relative to normal)	Number of Fragments (103 total)	Average GC Content	Average O/E Ratio	Percent that correspond to CpG Islands
Hypermethylated Fragments	Hyper-methylation	60	0.54	0.72	72%
Hypomethylated Fragments	Hypo-methylation	43	0.52	0.48	28%

Table II shows a summary of methylation pattern and sequence data for each *individual* sequence embodiment ([SEQ ID NOS:1-103]), corresponding to the 103 DNA fragments identified by MS.AP-PCR. Data for the 103 fragments was divided into either hypermethylated ([SEQ ID NOS:1-60]) or hypomethylated ([SEQ ID NOS:61-103])

5   categories. Table II also lists, for each sequence embodiment, the corresponding "Fragment Name," fragment "Size" (in base pairs; "bp"), "GC Content," Observed/Expected Ratio ("O/E Ratio"), "Description" (*i.e.*, as a CpG island if criteria are met), "Inventor Initials" (IDCM = Isabel D.C. Markl, JC = Jonathan Cheng, GL = Gangning Liang, HF = Hualin Fu, YT = Yoshitaka Tomigahara), "Cancer Source," and "Chromosome Match" to the GenBank

10   database. A dash ("-") indicates that no GenBank chromosome match existed, or that only a low-scoring partial match was found. Averages of the "GC Content" and "O/E Ratio," along with the percent of fragments that are CpG islands, are listed after the last member of both the hypermethylated and hypomethylated categories.

Therefore, the present invention provides for 103 DNA fragments and corresponding

15   marker sequence embodiments (*i.e.*, methylation-altered DNA sequences) that are useful in cancer prognostic, diagnostic and therapeutic applications.

Additionally, at least 55 of these 103 sequences correspond to CpG islands (based on GC Content and O/E ration); namely [SEQ ID NOS:2, 4, 6, 7, 9-16, 19, 20, 22-33, 35-43, 48, 51-55, 59, 60, 64, 71, 76, 78-81, 84 and 87-90]. Thus, based on the fact that the methylation

20   state of a portion of a given CpG island is generally representative of the island as a whole, the present invention further encompassed the novel use of the 55 CpG islands associated with [SEQ ID NOS:2, 4, 6, 7, 9-16, 19, 20, 22-33, 35-43, 48, 51-55, 59, 60, 64, 71, 76, 78-81, 84 and 87-90] in cancer prognostic, diagnostic and therapeutic applications, where a CpG island sequence associated with the sequence of a particular SEQ ID NO is that contiguous

25   sequence of genomic DNA that encompasses at least one nucleotide of the particular SEQ ID NO sequence, and satisfies the criteria of having both a frequency of CpG dinucleotides corresponding to an Observed/Expected Ratio >0.6, and a GC Content >0.5.

TABLE II. Summary of MS.AP-PCR Fragments Sequenced

Methylation Pattern	Fragment Name	Size (bp)	GC Content	O/E Ratio	Description	Inventor Initials	Cancer Source	Chromosome Matches	[SEQ ID NO]
Hyper-methylation Category	11-1A	510	0.44	0.74		IDCM	Bladder	-	1
	14-3B	313	0.58	0.74	CpG Island	IDCM	Bladder	2	2
	18-2B	165	0.57	0.45		IDCM	Bladder	7	3
	24-1B	601	0.51	0.72	CpG Island	IDCM	Bladder	Xp11	4
	26-1B	801	0.48	0.56		IDCM	Bladder	-	5
	26-2C	204	0.50	0.63	CpG Island	IDCM	Bladder	-	6
	30-3D	205	0.55	1.25	CpG Island	IDCM	Bladder	14	7
	32-3E	597	0.57	0.10		IDCM	Bladder	20q12-13.1	8
	34-2B	500	0.62	0.66	CpG Island	IDCM	Bladder	20	9
	34-4B	343	0.70	0.81	CpG Island	IDCM	Bladder	-	10

Methylation Pattern	Fragment Name	Size (bp)	GC Content	O/E Ratio	Description	Inventor Initials	Cancer Source	Chromosome Matches	[SEQ ID NO]
	34-5D	291	0.62	0.96	CpG Island	IDCM	Bladder	9	11
	34-6A	266	0.64	0.93	CpG Island	IDCM	Bladder	-	12
	35-1C	553	0.64	0.63	CpG Island	IDCM	Bladder	-	13
	36-2D	156	0.60	0.58	CpG Island	IDCM	Bladder	10	14
	38-1A	300	0.70	0.80	CpG Island	IDCM	Bladder	10	15
	38-2B	196	0.56	0.89	CpG Island	IDCM	Bladder	15	16
	7-8E	299	0.59	0.39		IDCM	Bladder	17q21-22	17
	83-4B	363	0.54	0.49		IDCM	Bladder	-	18
	84-1D	322	0.55	0.90	CpG Island	IDCM	Bladder	7	19
	101-3E	255	0.57	0.83	CpG Island	IDCM	Bladder	17	20
	M1-5A	406	0.45	0.96		IDCM	Bladder	1	21
	U2-8E	210	0.56	0.61	CpG Island	IDCM	Bladder	2	22
	U12-1A	310	0.56	0.81	CpG Island	IDCM	Bladder	2	23
	U7-4A	305	0.59	0.80	CpG Island	IDCM	Bladder	-	24
	NU9-5A	379	0.67	0.83	CpG Island	JC	Bladder	-	25
	3-17-8-B	625	0.48	0.72	CpG Island	GL	Bladder	18	26
	4-10-4-A	499	0.55	0.30	CpG Island	GL	Bladder	7	27
	1-1-1-A	561	0.58	0.98	CpG Island	GL	Bladder	20	28
	3-17-8-A	717	0.50	0.68	CpG Island	GL	Bladder	17	29
	G145-H	280	0.50	1.10	CpG Island	GL	Bladder	11	30
	1-1-1-D	270	0.50	0.60	CpG Island	GL	Bladder	2	31
	1-1-1-C	347	0.65	1.25	CpG Island	GL	Bladder	-	32
	G178-A	342	0.55	0.85	CpG Island	GL	Bladder	2	33
	34-A'	370	0.62	0.44		HF	Prostate	-	34
	34-D	213	0.53	0.74	CpG Island	HF	Prostate	2	35
	35-D	173	0.56	0.66	CpG Island	HF	Prostate	3	36
	36-A	369	0.67	0.70	CpG Island	HF	Prostate	-	37
	40-A	123	0.60	1.16	CpG Island	HF	Prostate	-	38
	91-1	450	0.64	0.86	CpG Island	YT	Bladder	5 or 16q24.3	39
	93-2	593	0.51	0.68	CpG Island	YT	Bladder	Xp11	40
	93-3	457	0.52	0.94	CpG Island	YT	Bladder	Xp22.1-22.3	41
	94-8	211	0.66	0.96	CpG Island	YT	Bladder	-	42
	95-5	141	0.63	0.79	CpG Island	YT	Bladder	14	43
	97-5	559	0.56	0.40		YT	Bladder	-	44
	98-1	433	0.46	0.96		YT	Bladder	1	45
	100-1	487	0.59	0.58		YT	Bladder	14	46
	100-2	403	0.60	0.47		YT	Bladder	3	47
	100-6	155	0.57	0.99	CpG Island	YT	Bladder	20	48
	4-2	256	0.57	0.40		YT	Bladder	7	49
	5-8	224	0.47	0.96		YT	Bladder	5	50
	6-4	313	0.70	0.82	CpG Island	YT	Bladder	-	51
	7-6	385	0.70	0.88	CpG Island	YT	Bladder	-	52
	13-3	307	0.59	0.89	CpG Island	YT	Bladder	10	53
	15-2	182	0.62	0.92	CpG Island	YT	Bladder	13	54
	23-2	523	0.54	0.87	CpG Island	YT	Bladder	Xp22.1-22.3	55
	39-2	795	0.46	0.64		YT	Bladder	13	56
	40-2	438	0.62	0.51		YT	Bladder	10	57
	41-3	611	0.47	0.70		YT	Bladder	18	58
	105-4	291	0.58	0.71	CpG Island	YT	Bladder	5	59
	107-8	226	0.53	0.96	CpG Island	YT	Bladder	11	60
AVERAGE			*0.54*	*0.72*	*72% islands*				
Hypo-methylation Category	14-2B	580	0.55	0.51		IDCM	Bladder	2	61
	16-1B	633	0.56	0.39		IDCM	Bladder	-	62
	18-1B	703	0.45	0.35		IDCM	Bladder	17	63

Methylation Pattern	Fragment Name	Size (bp)	GC Content	O/E Ratio	Description	Inventor Initials	Cancer Source	Chromosome Matches	[SEQ ID NO]
	19-1B	420	0.66	0.87	CpG Island	IDCM	Bladder	-	64
	20-1B	496	0.61	0.59		IDCM	Bladder	-	65
	21-2C	637	0.60	0.33		IDCM	Bladder	9q34	66
	29-1A	595	0.55	0.27		IDCM	Bladder	Xp11.23	67
	29-2B	580	0.47	0.77		IDCM	Bladder	-	68
	32-1A	589	0.59	0.48		IDCM	Bladder	-	69
	34-1B	450	0.42	0.46		IDCM	Bladder	-	70
	34-3B	432	0.70	0.61	CpG Island	IDCM	Bladder	-	71
	32-2B	748	0.47	0.24		IDCM	Bladder	2	72
	32-4B	599	0.57	0.15		IDCM	Bladder	20q12-13.1	73
	32-5B	614	0.58	0.20		IDCM	Bladder	-	74
	33-1A	552	0.54	0.32		IDCM	Bladder	10	75
	5-1E	501	0.61	1.04	CpG Island	IDCM	Bladder	-	76
	6-1A	826	0.55	0.36		IDCM	Bladder	22q13.32-13.33	77
	7-5D	433	0.59	0.85	CpG Island	IDCM	Bladder	5	78
	8-7C	424	0.58	0.83	CpG Island	IDCM	Bladder	5	79
	30-6D	285	0.63	0.72	CpG Island	IDCM	Bladder	1	80
	66-2E ·	401	0.54	0.82	CpG Island	IDCM	Bladder	16	81
	78-1C	268	0.54	0.41		IDCM	Bladder	-	82
	97-2E	989	0.53	0.16		IDCM	Bladder	-	83
	M1-8C	250	0.64	0.99	CpG Island	IDCM	Bladder	-	84
	M2-5A	402	0.50	0.45		IDCM	Bladder	5	85
	M1-4P	595	0.43	0.41		IDCM	Bladder	-	86
	M12-10A	304	0.53	0.76	CpG Island	IDCM	Bladder	7	87
	M12-12C	296	0.51	0.64	CpG Island	IDCM	Bladder	17	88
	M2-8M	220	0.67	0.62	CpG Island	IDCM	Bladder	6q27	89
	NU4-3A	273	0.63	1.02	CpG Island	JC	Bladder	-	90
	NU5-2A	361	0.44	0.73		JC	Bladder	6q14.3-15	91
	88-5	462	0.62	0.39		YT	Bladder	-	92
	90-1	591	0.66	0.45		YT	Bladder	19	93
	91-3	279	0.58	0.45		YT	Bladder	5 or 16q24.3	94
	91-4	351	0.55	0.30		YT	Bladder	18q23	95
	91-7	171	0.61	0.59		YT	Bladder	11	96
	89-3	743	0.55	0.43		YT	Bladder	-	97
	94-2	589	0.53	0.41		YT	Bladder	22q13.31-13.32	98
	94-3	538	0.53	0.49		YT	Bladder	5 or 18	99
	94-4	486	0.61	0.57		YT	Bladder	-	100
	94-5	450	0.60	0.45		YT	Bladder	1p36.2-36.3	101
	94-6	292	0.58	0.32		YT	Bladder	8 or 9	102
	96-4	395	0.63	0.54		YT	Bladder	9	103
AVERAGE			0.52	0.48	28% islands				

Diagnostic and Prognostic Assays for Cancer. The present invention provides for diagnostic and prognostic cancer assays based on determination of the methylation state of one or more of the disclosed 103 methylation-altered DNA sequence embodiments. Typically, such assays involve obtaining a tissue sample from a test tissue, performing a methylation assay on DNA derived from the tissue sample, and making a diagnosis or prognosis based thereon.

The methylation assay is used to determine the methylation state of one or a plurality of CpG dinucleotide within a DNA sequence of the DNA sample. According to the present invention, possible methylation states include *hypermethylation* and *hypomethylation*, relative to a normal state (*i.e.*, non-cancerous control state). Hypermethylation and hypomethylation

5   refer to the methylation states corresponding to an *increased* or *decreased*, respectively, presence 5-methylcytosine ("5-mCyt") at one or a plurality of CpG dinucleotides within a DNA sequence of the test sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

A diagnosis or prognosis is based, at least in part, upon the determined methylation

10   state of the sample DNA sequence compared to control data obtained from normal, non-cancerous tissue.

Methylation Assay Procedures. Various methylation assay procedures are known in the art, and can be used in conjunction with the present invention. These assays allow for determination of the methylation state of one or a plurality of CpG dinucleotides (*e.g.*, CpG

15   islands) within a DNA sequence. Such assays involve, among other techniques, DNA sequencing of bisulfite-treated DNA, PCR (for sequence-specific amplification), Southern blot analysis, use of methylation-sensitive restriction enzymes, etc.

For example, genomic sequencing has been simplified for analysis of DNA methylation patterns and 5-methylcytosine distribution by using bisulfite treatment (Frommer

20   et al., *Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). Additionally, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is used, *e.g.*, the method described by Sadri & Hornsby (*Nucl. Acids Res.* 24:5058-5059, 1996), or COBRA (Combined Bisulfite Restriction Analysis) (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997).

25   *COBRA.* COBRA analysis is a quantitative methylation assay useful for determining DNA methylation levels at specific gene loci in small amounts of genomic DNA (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997). Briefly, restriction enzyme digestion is used to reveal methylation-dependent sequence differences in PCR products of sodium bisulfite-treated DNA. Methylation-dependent sequence differences are first introduced into the

30   genomic DNA by standard bisulfite treatment according to the procedure described by Frommer et al. (*Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). PCR amplification of the bisulfite converted DNA is then performed using primers specific for the interested CpG islands, followed by restriction endonuclease digestion, gel electrophoresis, and detection using specific, labeled hybridization probes. Methylation levels in the original DNA sample

35   are represented by the relative amounts of digested and undigested PCR product in a linearly quantitative fashion across a wide spectrum of DNA methylation levels. In addition, this technique can be reliably applied to DNA obtained from microdissected paraffin-embedded tissue samples. Typical reagents (*e.g.*, as might be found in a typical COBRA-based kit) for

COBRA analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); restriction enzyme and appropriate buffer; gene-hybridization oligo; control hybridization oligo; kinase labeling kit for oligo probe; and radioactive nucleotides. Additionally, bisulfite conversion reagents may include:

5 DNA denaturation buffer; sulfonation buffer; DNA recovery regents or kit (*e.g.*, precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

Preferably, assays such as "MethyLight" (a fluorescence-based real-time PCR technique) (Eads et al., *Cancer Res*. 59:2302-2306, 1999), Ms-SNuPE (Methylation-sensitive

10 Single Nucleotide Primer Extension) reactions (Gonzalgo & Jones, *Nucleic Acids Res*. 25:2529-2531, 1997), methylation-specific PCR ("MSP"; Herman et al., *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146), and methylated CpG island amplification ("MCA";Toyota et al., *Cancer Res*. 59:2307-12, 1999) are used alone or in combination with other of these methods.

15 *MethyLight*. The MethyLight assay is a high-throughput quantitative methylation assay that utilizes fluorescence-based real-time PCR (TaqMan ®) technology that requires no further manipulations after the PCR step (Eads et al., *Cancer Res*. 59:2302-2306, 1999). Briefly, the MethyLight process begins with a mixed sample of genomic DNA that is converted, in a sodium bisulfite reaction, to a mixed pool of methylation-dependent sequence

20 differences according to standard procedures (the bisulfite process converts unmethylated cytosine residues to uracil). Fluorescence-based PCR is then performed either in an "unbiased" (with primers that do not overlap known CpG methylation sites) PCR reaction, or in a "biased" (with PCR primers that overlap known CpG dinucleotides) reaction. Sequence discrimination can occur either at the level of the amplification process or at the level of the

25 fluorescence detection process, or both.

The MethyLight may assay be used as a quantitative test for methylation patterns in the genomic DNA sample, wherein sequence discrimination occurs at the level of probe hybridization. In this quantitative version, the PCR reaction provides for unbiased amplification in the presence of a fluorescent probe that overlaps a particular putative

30 methylation site. An unbiased control for the amount of input DNA is provided by a reaction in which neither the primers, nor the probe overlie any CpG dinucleotides. Alternatively, a qualitative test for genomic methylation is achieved by probing of the biased PCR pool with either control oligonucleotides that do not "cover" known methylation sites (a fluorescence-based version of the "MSP" technique), or with oligonucleotides covering potential

35 methylation sites.

The MethyLight process can by used with a "TaqMan®" probe in the amplification process. For example, double-stranded genomic DNA is treated with sodium bisulfite and subjected to one of two sets of PCR reactions using TaqMan® probes; *e.g.*, with either

biased primers and TaqMan® probe, or unbiased primers and TaqMan® probe. The TaqMan® probe is dual-labeled with fluorescent "reporter" and "quencher" molecules, and is designed to be specific for a relatively high GC content region so that it melts out at about 10 °C higher temperature in the PCR cycle than the forward or reverse primers. This allows the

5 TaqMan® probe to remain fully hybridized during the PCR annealing/extension step. As the Taq polymerase enzymatically synthesizes a new strand during PCR, it will eventually reach the annealed TaqMan® probe. The Taq polymerase 5' to 3' endonuclease activity will then displace the TaqMan® probe by digesting it to release the fluorescent reporter molecule for quantitative detection of its now unquenched signal using a real-time fluorescent detection

10 system.

Typical reagents (e.g., as might be found in a typical MethyLight-based kit) for MethyLight analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); TaqMan® probes; optimized PCR buffers and deoxynucleotides; and Taq polymerase.

15 *Ms-SNuPE*. The Ms-SNuPE technique is a quantitative method for assessing methylation differences at specific CpG sites based on bisulfite treatment of DNA, followed by single-nucleotide primer extension (Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997). Briefly, genomic DNA is reacted with sodium bisulfite to convert unmethylated cytosine to uracil while leaving 5-methylcytosine unchanged. Amplification of the desired

20 target sequence is then performed using PCR primers specific for bisulfite-converted DNA, and the resulting product is isolated and used as a template for methylation analysis at the CpG site(s) of interest. Small amounts of DNA can be analyzed (e.g., microdissected pathology sections), and it avoids utilization of restriction enzymes for determining the methylation status at CpG sites. Typical reagents (e.g., as might be found in a typical Ms-

25 SNuPE-based kit) for Ms-SNuPE analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); optimized PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for specific gene; reaction buffer (for the Ms-SNuPE reaction); and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer;

30 sulfonation buffer; DNA recovery regents or kit (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

MSP. MSP (methylation-specific PCR) allows for assessing the methylation status of virtually any group of CpG sites within a CpG island, independent of the use of methylation-sensitive restriction enzymes (Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996;

35 US Patent No. 5,786,146). Briefly, DNA is modified by sodium bisulfite converting all unmethylated, but not methylated cytosines to uracil, and subsequently amplified with primers specific for methylated versus unmethylated DNA. MSP requires only small quantities of DNA, is sensitive to 0.1% methylated alleles of a given CpG island locus, and

can be performed on DNA extracted from paraffin-embedded samples. Typical reagents (e.g., as might be found in a typical MSP-based kit) for MSP analysis may include, but are not limited to: methylated and unmethylated PCR primers for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes.

MCA. The MCA technique is a method that can be used to screen for altered methylation patterns in genomic DNA, and to isolate specific sequences associated with these changes (Toyota et al., *Cancer Res.* 59:2307-12, 1999). Briefly, restriction enzymes with different sensitivities to cytosine methylation in their recognition sites are used to digest genomic DNAs from primary tumors, cell lines, and normal tissues prior to arbitrarily primed PCR amplification. Fragments that show differential methylation are cloned and sequenced after resolving the PCR products on high-resolution polyacrylamide gels. The cloned fragments are then used as probes for Southern analysis to confirm differential methylation of these regions. Typical reagents (e.g., as might be found in a typical MCA -based kit) for MCA analysis may include, but are not limited to: PCR primers for arbitrary priming Genomic DNA; PCR buffers and nucleotides, restriction enzymes and appropriate buffers; gene-hybridization oligos or probes; control hybridization oligos or probes.

Kits for Detection of Methylated CpG-containing Nucleic Acid. The reagents required to perform one or more art-recognized methylation assays (including those identified above) are combined with primers or probes comprising the sequences of SEQ ID NOS:1-103, or portions thereof, to determine the methylation state of CpG-containing nucleic acids. For example, the MethyLight, Ms-SNuPE, MCA, COBRA, and MSP methylation assays could be used alone or in combination, along with primers or probes comprising the sequences of SEQ ID NOS:1-103, or portions thereof, to determine the methylation state of a CpG dinucleotide within a genomic sequence corresponding to SEQ ID NOS:1-103, or to CpG island sequences associated with sequences of SEQ ID NOS:1-103, where the CpG island sequence associated with the sequence of the particular SEQ ID NO is that contiguous sequence of genomic DNA that encompasses at least one nucleotide of the particular SEQ ID NO sequence, and satisfies the criteria of having both a frequency of CpG dinucleotides corresponding to an Observed/Expected Ratio >0.6, and a GC Content >0.5.

We claim:

1.   A diagnostic or prognostic assay for cancer, comprising:

(a)   obtaining a tissue sample from a test tissue;

(b)   performing a methylation assay on DNA derived from the tissue sample,
wherein the methylation assay determines the methylation state of a CpG dinucleotide within
a DNA sequence of the DNA, and wherein the DNA sequence is a sequence selected from
the group consisting of sequences of SEQ ID NOS:1-103, sequences having a nucleotide
sequence at least 90% identical to sequences of SEQ ID NOS:1-103, CpG island sequences
associated with sequences of SEQ ID NOS:1-103, CpG island sequences associated with
sequences having a nucleotide sequence at least 90% identical to sequences of SEQ ID
NOS:1-103, and combinations thereof, wherein the CpG island sequence associated with the
sequence of the particular SEQ ID NO is that contiguous sequence of genomic DNA that
encompasses at least one nucleotide of the particular SEQ ID NO sequence, and satisfies the
criteria of having both a frequency of CpG dinucleotides corresponding to an
Observed/Expected Ratio >0.6, and a GC Content >0.5; and

(c)   determining a diagnosis or prognosis based, at least in part, upon the
methylation state of the CpG dinucleotide within the DNA sequence.

2.   The diagnostic or prognostic assay of claim 1 wherein the DNA sequence is a
sequence selected from the group consisting of CpG island sequences associated with
sequences of SEQ ID NOS:1-103, CpG island sequences associated with sequences having a
nucleotide sequence at least 90% identical to sequences of SEQ ID NOS:1-103, and
combinations thereof.

3.   The diagnostic or prognostic assay of claim 2 wherein the DNA sequence is a
sequence selected from the group consisting of CpG island sequences associated with
sequences of SEQ ID NOS: 2, 4, 6, 7, 9-16, 19, 20, 22-33, 35-43, 48, 51-55, 59, 60, 64, 71,
76, 78-81, 84 and 87-90, and combinations thereof.

4.   The diagnostic or prognostic assay of claim 1 wherein the methylation assay
procedure is selected from the group consisting of MethyLight, MS-SNuPE, MSP MCA,
COBRA, and combinations thereof.

5.   The diagnostic or prognostic assay of claim 1 wherein the methylation state of
the CpG dinucleotide within the DNA sequence is that of hypermethylation, hypomethylation
or normal methylation.

6.   The diagnostic or prognostic assay of claim 1 wherein the cancer is selected
from the group consisting of bladder cancer, prostate cancer, colon cancer, lung cancer, renal
cancer, leukemia, breast cancer, uterine cancer, astrocytoma, glioblastoma, and
neuroblastoma.

7.   A kit useful for the detection of a methylated CpG-containing nucleic acid
comprising a carrier means containing one or more containers comprising:

(a) a container containing a probe or primer which hybridizes to any region of a
sequence selected from the group consisting of SEQ ID NOS:1-103, and sequences having a
nucleotide sequence at least 90% identical to sequences of SEQ ID NOS:1-103; and

(b) additional standard methylation assay reagents required to affect detection of
5   methylated CpG-containing nucleic acid based, at least in part, on the probe or primer.

8.   The kit of claim 7, wherein the additional standard methylation assay reagents
are standard reagents for performing a methylation assay from the group consisting of
MethyLight, MS-SNuPE, MSP MCA, COBRA, and combinations thereof.

9.   The kit of claim 7, wherein the probe or primer comprises at least about 12 to
10 15 nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1-103, and
sequences having a nucleotide sequence at least 90% identical to sequences of SEQ ID
NOS:1-103.

10.   An isolated nucleic acid molecule comprising a methylated or unmethylated
polynucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5,
15 SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:18, SEQ ID
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20 NO:86, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:97, and SEQ ID NO:100.

11.   The nucleic acid of claim 10, wherein the nucleic acid is methylated.

12.   The nucleic acid of claim 10, wherein the nucleic acid is unmethylated.

SEQUENCE LISTING

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      Markl, Isabel
      Tomigahara, Yoshitaka
      Liang, Gangning
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gaatggcctc taatctcggt gttaaatact ttatgagagt atcaatacca cctaatcctt     120

tgctgagaat tactgctaga aatgtagatt ctgaggttcc gaaagtttgt ttttggttac     180

cccctccagc tcctcccgcg gcaa                                            204
```

```
<210>  7
<211>  205
<212>  DNA
<213>  Homo sapiens

<400>  7
agacctttat cgggcgtgag tgaaatcggt cgttcgtgtt tttcgtgggt cttccaacca      60

caggccgcct gagatggttc tagtcccttt gagtatacag acccttcctg tgcattgacc     120

gacacagctc ggcccggatc ccgaaatgaa cgtttctacc ttcggaacgc tgcgtctcgg     180

atccttctga acccgcacgt cgcaa                                           205
```

```
<210>    8
<211>    597
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 361 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 382 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 513 nucleotides
<223>    "n" refers to an undetermined base


<400>    8
gaccatgaaa tcgtgtggct ctagcccctt ctgggcctct tgttggtaat gaagccactc      60

taaagcgccc cctgttattc agagggctcc ccagctgcca tgatatgtgt atggggaggg     120

catagcaggt ccttttgccc cggcagccat tcttctgctc acaaggggct ggctctgggg     180

acagggatgt ctttgtcatc agtgaccact aatccccctc ctcattggcc tccagggctg     240

ctccccttca ctctcttggt tgaagttgta ggggctgagg ttaccctgag aaacacctgt     300

tcttggagcc catagaccca accttggaga tgcaggggga gccactggct gggctctgca     360

ngtggggcca gctgatcccc anctgctggc acctccaggc atccacagag cttggagtcc     420

cagccacatt tcctccttgg ccttagaggg agaggaagtc ctttgattgc ctagtccaag     480

atccctttat ttcctgccct gggattatgg ggnagcaagc catgcccttc atgggaagct     540

gttctccctt cctcggggtt gggtctggcc tcagctcggg caacagtcat gatgggc       597


<210>    9
<211>    500
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 10 nucleotides
<223>    "n" refers to an undetermined base


<400>    9
```

```
gccaaacgcn ataccctctg cggggtgaga atgcgggccc gcccggctcc tcccgtgagg      60

ccagggcctc ctgttctcct agacacccca aggagccaac tcctccgcag aagttccccg     120

cttctgctct tatttccaag cttcgcgctt tctacaaact ccctgttgcc ttgactttga     180

tttccagccg tggtgagggt cagagtgaac cccggcgcgc tccccgacgg catccccgca     240

caccaggata ggagaaattg gagggcctgg ggcctcgggc tccgcagtcg tcggaggaag     300

aacccaccgc ggggtccgca agggaaagtg aagaggcccg ggattttttcc aaagcgctgg    360

ccaggacccc gaaggaaggg gaggagtcac ctgaagccgg ggaaggcccc ttgggtgctc     420

tgccttggat ccttatgttc actgactttc gcgacccctg gagggggggca aatccgcgct    480

gtttcccccca acttggcttc                                               500
```

```
<210>  10
<211>  343
<212>  DNA
<213>  Homo sapiens

<400>  10
gccaacccac accagtacct gggaccgggg ggagcccggt ccggccgcta aaccgggctg      60

gctggcgcca gggctccggg aggtgcggtc cggcgggggaa gccgtgatgg gaagcgactc     120

tgtccaggga gtgtccttca ccaccacact cctcacgtcc aggcagtgat cgacggcctg     180

gcggcaccct cacagcgggc ccatagcacg gggccacaca cgtcccctga gcttagcctg     240

ggcacattcg tctgccgccg agggcttaag ccagtctgca gcccgcgccc cgtcactcgg     300

acgcaagtcc gtcgtccgct ctgccacgcg gccgctaagc cga                      343
```

```
<210>  11
<211>  291
<212>  DNA
<213>  Homo sapiens

<400>  11
gtcctacaca ctccgcacac aacgcggccg gtgttaagtc tccaaacgcc ccgagagctc      60

caaggaccgc gcgcgcgaag gcgccgtagc aagtgggcac acaccagaca ccacccccggc    120

gtgttccgcg ggagaagcca gtgcacacat cctcccgcaa ggcggggttg ccagtgcaac     180

acaggaatcc tgcccttttt ctagaaaagc cccctccccc actttccctc caatacactc     240

acctgcgtct caacagtttc cttcttgcgc tacacgcggc cgctaagccg a             291
```

```
<210>  12
<211>  266
```

6

<212> DNA
<213> Homo sapiens

<400> 12
gtccggatca gtttccccgg ccaggtcgct tcccggtctc aaccatttcg cgctctgctc   60

tgtccgctgg tttgtccctg cccggttcct ctccccgggc ctgtcagcct ccgcttctct   120

ggaggttcct gggactcatc tctgatccac cgtcttgcgt tctctgggcg catcgacttc   180

tctccatctt cgggctcact cctgactccc tcgctgccgc ccccgggggt ttccacgcgt   240

gtctctaacc gcggccgcta agccga   266

<210> 13
<211> 553
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 497 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 513 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 517 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 519 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 527 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 546 nucleotides
<223> "n" refers to an undetermined base

<400> 13
gatcctggtc catcgaaacc ttgtgtgcat cggttagtgc ttcctgggcg tttgcttcta   60

gccgacgctg acagtggagt gccagaaaga gggagaggac cgtcatggct actctgcccc   120

tggtgtcacc atgcgctctc ccccggcacc ggcgaggcga aacgtttcgc tagtccccgg   180

```
gaggcccctc ggtcagggca gcagcatccc tgcaccctct ccgcaggtgg tctccccgac    240

gccacaggtg gccagcaggg cgcgggtggg ggcaggagcg cctctcccct gcccaggcct    300

cccgctcctt ctcggagcgc tgtggcgggg tggagagaca gccttctaca gctagtctag    360

ctcggcgcgg ttcccgtctg tggcctccta atcccacagc cacagcgcct tcctctaacc    420

tccctcggtg ggcttaaagc ctcccgttcc ttctgtctca ttccttctgc tccctccccc    480

cgaaacccccc agatganagc tgggaacctg gcnccantna ctgagcnaac agtgttgacg    540

ggccgnggcc caa                                                       553
```

```
<210>    14
<211>    156
<212>    DNA
<213>    Homo sapiens

<400>    14
gcgcacacag tgggtacaag gatgagctcg gtgtaaggaa tggaaagccc ccagtctaaa     60

ccaccgcccc ctagacacgg gtgaaaacct gcctaaaagc taactcaggc agtgactcta    120

tcacccgaag gggccctggg ccgcggccca agccga                              156
```

```
<210>    15
<211>    300
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 117 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 154 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 163 nucleotides
<223>    "n" refers to an undetermined base

<400>    15
gttcacagcc cataaggtgg gggtggcccg aacctgaaac ggagcctgag ccaggatcct     60

gcaaccaaag tctgaagcgc cccccggtgg gggccgagag cgctgcaggc aggtggnggc    120

gcggggcagg cgggcgggcg aagggagctc cggntacgca ganaacgcgg agcgccccct    180
```

tcccacctgc gcgagggcat cctgcccggg ggaggaaagg cgggagtccg aggcgggtcg   240

gattcccagc cagctccctc ctcacaggag gcggcccatt atccggcgtc gcaaagccga   300

<210> 16
<211> 196
<212> DNA
<213> Homo sapiens

<400> 16
ggcgcccagc aggggagcga gggaggaggg tgcagaaaga ggctccgaaa ttgggggaaa   60

ctgacccgtg cttctctacc ttcggaggtg ggacagttgc acgaagtgct agttagaccg   120

gatcagttgg aactgacgga ggactgcaaa gaagaaacta aaatagacgt cgaaagcctg   180

tcctcggcgt cgcaaa   196

<210> 17
<211> 299
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 21 nucleotides
<223> "n" refers to an undetermined base

<400> 17
acaccaggag aggggaagaa nccagcacct accgacaggg gtggagctgg gtcaagaatg   60

gtgtggtccc tgctttgggg gaatgctggg gaggtagaaa gccccttcta acggggcgtc   120

actgcaatta ctgcttcctc tttcccataa aactccccct agtgtatcag aacccccaag   180

gagtttcagt aagcggttct tctgttgtct ccggctgaga ctccagggga acctcaagct   240

cacatggccc tggccgggcc cctgggcagg agcaggcgag aggtctgcgc ggccgctaa   299

<210> 18
<211> 363
<212> DNA
<213> Homo sapiens

<400> 18
gggtatgtgt tacacatccg agataactac acaggcatcg accctgtcca cccggggatg   60

ctagaggggc tgcgctggtt ttactccagg ccatggtgag agccaccgtg aacacagggc   120

tctctcctct gagctgcaga agctctgtgc cctgtcccct gccacaagtc acagactttc   180

ttcatgtgtt ttacctcatg ttaatgaagg agatcttctc cagggggcttg atctagtggg   240

```
aaacagagga gggggggatt ttaaatttca gtccgtccaa ccctgtagat ctgctgtcct      300

acagtaacgt aaaggatcac caggtaaaac gctgcttctc ccggacgccg ccccgcaagc      360

cga                                                                    363
```

```
<210>  19
<211>  322
<212>  DNA
<213>  Homo sapiens

<400>  19
ccggcccgtc cctcttaata tggcctcagt tccgaaaacc acagaataga accgcggtcc       60

tattccatta ttcctagctg aggtatccag gcggctcgga cctgctttga acactctaat      120

tttttcaaag taaacgcttc gggctgcagg acactcagct aagagcatca ggggggcgcc      180

aagaggcaag gggcggggat gggtggtggc tcgcctcgtg gcagaccgcc cgcccgctcc      240

caagatccaa ctacgagctt tttaactgca gcaactttaa tatacgctat tggagctgga      300

attaccgcgg ccgctaagcc ga                                               322
```

```
<210>  20
<211>  255
<212>  DNA
<213>  Homo sapiens

<400>  20
taataagata ccaaatcggg cgagaaacga aaagctcctg gcctccgtat ttggggccag       60

agacaccgca gggagtcagg tccccgccga caaatcggaa gaggcctgcg ggagttagcc      120

agataatgct ctccctgtcc tacccgtccc caccaatttg ccttttacct gccgcagagc      180

ttgcttgaac caaagggggtt tgcggtcttc tcctcctcaa cttgcgatcc ccaggccttc      240

gcgtcccgaa gccga                                                       255
```

```
<210>  21
<211>  406
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 6 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 7 nucleotides
<223>  "n" refers to an undetermined base
```

10

<220>
<221> unsure
<222> position is 18 nucleotides
<223> "n" refers to an undetermined base

<400> 21
atgtgnnaag gctcgctntc catttctctt ttcctccttc tccctctctc atgtgcggtc   60

tccctcaaca tccaaaccaa ccgagtgcgt ctgaggtgaa atcgtgccag acttagagac   120

ggctgccagg tttctctcaa gtcttggctt aacaaaagaa agcaaattac aaaaatggaa   180

attttcaaac tagcgttcag tggtattcaa atcgacgttt gggtagcgca caggcacaga   240

ccgcattcgt gctattttgt gattaaaatg ataccaaaaa tacctccttg ctttggtttt   300

cgtcttcgaa aacgacttct ttccttcttc taatttcccc cttactttg ggagcggcaa   360

accctgacc actctagaat tgctaacatt tggaccggcg tcgcaa   406

<210> 22
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 10 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 13 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 14 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 25 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 40 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 46 nucleotides
<223> "n" refers to an undetermined base

```
<220>
<221>  unsure
<222>  position is 47 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 50 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 76 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 95 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 207 nucleotides
<223>  "n" refers to an undetermined base


<400>  22
gcacgttcgn gcnncgtgta ccatnagctg ccaactggan gcaccnnggn aagggtgggg      60

gcctcctgga gacttngggg agagggatag ccggntaaag ctcctgtcct ttctataggc     120

ataagcgggt ggtcaccacg gattggggat cccgaatccc tggctccaga tagacttaat     180

gaagaagcac ctggatccgg gccgcgncaa                                      210


<210>  23
<211>  310
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 9 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 11 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 32 nucleotides
<223>  "n" refers to an undetermined base
```

<220>
<221> unsure
<222> position is 79 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 80 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 120 nucleotides
<223> "n" refers to an undetermined base

<400> 23
tcacgcttnc naaggctctg aatcctgagg gncagatctc caagaaggag ggaggctggt   60

cctagttccc gaggtcctnn actaggtcta gatcactggg taaaagaagg ggagcggcan   120

cacgtatggg gtaggcgctc tcactactca catctcgaga cctttgccgg cgtagggctg   180

tccggggggga acgacccgcc ttttccggta tcggttgtca tggcggcgcc cagcccagcc   240

tggttttttc cggtagccaa ttgaactaac aaccccgttc cctttaggac taatctgtca   300

cgtcggcgca   310

<210> 24
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 13 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 74 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 266 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 269 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure

<222> position is 292 nucleotides
<223> "n" refers to an undetermined base

<400> 24
ctctggtctg tgntggatac gcgtgttctt ctgcggagtt aaagggtcgg ggacgggggt   60

tctggactta ccanagcaat tccagccggt gggcgtttgg cagtcactta aggaggtagg   120

gaaagcagcg agcttcaccg ggcgggctac gatgagtagc atgacgggca gcagcagcag   180

ccagcaaaag ccctcgcaaa gtgtccagct gctgcactgc cgcgggggact cccacagcac   240

catgactagt tcgtgcgact ctgcancanc aaacggcttc cgaggaacac angatcgcgg   300

gggca   304

<210> 25
<211> 379
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 6 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 10 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 13 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 19 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 21 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 31 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 113 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 184 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 206 nucleotides
<223> "n" refers to an undetermined base

<400> 25
aaaacncatn tgnagagcnc ntcggcagag ncgcagctgg ctgacccagg agaaggcgcg   60

ctgggtgtgg ctgggacggc caaggccgcg gcttcccgcg tggggatgcg ctntggcgca   120

aagctggtcc cggcgggggcc aggcgtttgt gggcgggtga cggggatcta gggcttccgc   180

tcgngattcc tcttgggctg tctttncggg tttggactcg cctgccaggc tgtgtgcagg   240

gttcccgctg cctctggccg gcaggcgtcc gggctgcagg tgggccggca ggcaggtgtt   300

agcgggaagg gagcacaggt agcgaggtgg gatcggcgac ctggctaggg tgtcggcaga   360

atggaatgcg cggccgcta   379

<210> 26
<211> 625
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 8 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 18 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 50 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 64 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 609 nucleotides
<223> "n" refers to an undetermined base

```
<220>
<221>  unsure
<222>  position is 616 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 618 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 621 nucleotides
<223>  "n" refers to an undetermined base


<400>  26
gggacgcnag ccaggggantt tgatccgttt tgaatgaaaa gaaagagaan ccaaaccaaa      60

cctntcagtc atccaaaacc ttcaggcttc cagggaggtt ttgctataat tttctctaag     120

catgactgtt tctgggggag gggaaagggg tggttgtatt tactgaaaat tcaaatcgaa     180

ataataaatg gccaaatttg gacacttacg gacccaaaca gttttgctca cgccagagaa     240

accgagagca cagggcttgc gtgaagccta tctcggcaga aggcaacatt ctaataaagc     300

ccgtgggaaa acagattaca ttttcgccat gaataagtca tgcagtgaaa aatattgcct     360

acagcctgtc gacttatatt attatcacgt ttttcaactc ggcgtgagga gggagaggag     420

tgttcatatt tgactaggaa ttgcaggatc gatgcaaact ccagggcagc agccagactg     480

gcatatgtgg ggctctccgg ttactttctc tgtatgtcgc gggtgagagg aacagcgagg     540

acaatttagc gcaaacacac gaagggtcgg atctcaaggg ggcagcgctg ggagaaaggt     600

tagggctgna gagcgnanag ncaaa                                           625


<210>  27
<211>  499
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 2 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 7 nucleotides
<223>  "n" refers to an undetermined base
```

```
<400>  27
gnctccncgt tcccctcggg cggaacggag gcaacttttcc ggagtctatt tttgttaaga     60

caatcaactc caataactga gctgaagttt ttgtttaaaa agaaaaaaat ctgataagtg    120

atgattttac ctacttgtgg acactagatt tcaattagga aggttttttt aaacggcttt    180

ttgtaacttc gctgcaggaa gcaggtttgt ttctttttct tttctttttta agagaaggtg    240

tatttcactg gtgcaatggc ttggcacctc cggggcctgg gaggacctca gacctcccca    300

gccctgggtt tctccgtctt caagaccaac taggaagggt caagcgggga gagggagtgg    360

agggtcaggt gagatctcag agctgccccg gccggccccc gtctctttct acctcctctt    420

ccagagaacc agcggctcac acccttctca acgcaggaca tgctcggcgg ccaaagccga    480

attctgcaga tatccatca                                                 499
```

```
<210>  28
<211>  561
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 20 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 21 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 23 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 26 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 39 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 40 nucleotides
<223>  "n" refers to an undetermined base

<220>
```

```
<221>  unsure
<222>  position is 44 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 49 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 65 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 80 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 98 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 107 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 471 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 484 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 544 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 559 nucleotides
<223>  "n" refers to an undetermined base


<400>  28
gggcgattgt tattcaaacn ngntanctct ctgcggggnn gagnaatgng ggcctcgcac     60

ggctncatcc ccgtcgagcn cagggcctcc ctgttctnct agacatncca aggagccaac     120

tcctccgcag aagttccccg cttctgctct tatttccaag cttcgcgctt tctacaaact     180
```

```
ccctgttgcc ttgactttga tttccagccg tggtgagggt cagagtgaac cccggcgcgc    240

tccccgacgg catccccgca caccaggata ggagaaattg gagggcctgg gcctcggctc    300

ccgcagtcgt cggaggaaga acccaccgcg gggtccccaa gggaaagtga agaggcccgg    360

gattttttcca aagcgctgcc aggaccccga aggaaggggga ggagtcacct gaagccgggg   420

aagctccttg ggtgctctcc ttggatcctt atgttcactg actttcgcga ngcccctgg     480

aggnggaaaa tccgcgctgt ttcccccaac ttaacttcac gcggccgcta agccgaattc    540

tgcngaaatc attacactng c                                            561
```

```
<210>   29
<211>   717
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 643 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 651 nucleotides
<223>   "n" refers to an undetermined base


<400>   29
actctccgcg gtntcntggt gcctcacagg aggtggggct ccctccaccc ggtccccagg     60

cctctccctc tgcccgagct tcccggtcct gcctccttcg cctcgcctgc ctgcccgact    120

ctgaaccctg ctcctcttct aactaaaagt cagtgtttta tttcctccgc agtccaatgc    180

ccgcgtttta ccttattcaa taagaagggc ttcatttatg gcaagacagg acagccaggt    240

aataagggcc tctgcacacg cgggcccatt ggaggggcgg aactgcgaag tcttcccgga    300

agagcttcct ggagagaagg ggaacgagcc agcgtttatt gagcatctat tatactaagc    360

atctgcttgg cagttcacga cggtcgcatt ttttcatcct tacagcgatc cctattgtgt    420

cgcttgcttt aaagcctcac agctcacaaa gggctgggat ttattccaga tctctctctc    480

agatgccatc tcacttccag gtgtctctgc tgctttgaac gcgggaaacc cacgcaaagg    540

agtgatttcc aaggccttct gtttggaata tctttaatcc tccccttatt aactggaaaa    600

actcccacgc atccttcagg gctcagctca aatgtccttt atntctgcag ngaaactttc    660

ccaaggaaaa ttagttacac agctaatttt agataaattg agccagttga tagaatt        717
```

19

```
<210>   30
<211>   280
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 30 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 189 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 192 nucleotides
<223>   "n" refers to an undetermined base


<400>   30
tgatggatat ctgcagaatt cgggctttgn gacgccgggc acgcagtagg gaaaacagta        60

ttaaaacgcc ctacagaaaa tctcggcgaa gtccccggag aactctggtt tctaagatca       120

gctgggcgca ctttctccgg gacgtccctt cttctcggtc tcagcgcctt cctgccctca       180

gccgcgccng tnttgttttg gtggcaaact gaaataagaa atggaaatat attggccttt       240

gctgctgcca gggatgagag gttgttgacg tcggcgcaaa                             280


<210>   31
<211>   270
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 2 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 5 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 6 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 8 nucleotides
<223>   "n" refers to an undetermined base
```

```
<220>
<221> unsure
<222> position is 9 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 11 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 12 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 24 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 26 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 27 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 29 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 33 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 36 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 227 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 244 nucleotides
<223> "n" refers to an undetermined base

<220>
```

```
<221>    unsure
<222>    position is 245 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 264 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 265 nucleotides
<223>    "n" refers to an undetermined base


<400>    31
gnggnngnna nncggcgatg gatntnngna ganttnggtg atggatatct gcagaattcg      60

gcttagcggc cgcgaacaaa gagcgaacca aaggatgctt cgaattttta aaacggaatc     120

tctgcaccca aatgcaggac tggtgactta aggagctgcg aagtctgatt taccgggcct     180

actctcgacc tgcccccac ccccagctca gggggacctt tttatcntga acgccagagc      240

tacnnaccaa gtcgggtggc cacnnccaaa                                      270


<210>    32
<211>    347
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 7 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 8 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 11 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 50 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 309 nucleotides
<223>    "n" refers to an undetermined base
```

<220>
<221> unsure
<222> position is 313 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 322 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 325 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 331 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 336 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 337 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 338 nucleotides
<223> "n" refers to an undetermined base

<400> 32
tttggannta nggggggcgtg gcgtggatcc agtttcccc ggccaggtcn gcttcccggt   60

ctcaaccatt tcgcgctctg ctctgtccgc tggtttgtcc ctgcccggtt cctctccccg   120

ggcctgtcag cctccgcttc tctggaggtt cctgggactc atctctgatc caccgtcttg   180

cgttctctgg gcgcatcgac ttctctccat cttcgggctc actcctgact ccctcgctgc   240

cgccccgggg gtttccacgc gtgtctctaa ccgcggccgc taagccgaat tctgcagata   300

tccatcacng aantctgcag anatncatcg ncgaannnca ccgcact   347

<210> 33
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 193 nucleotides

```
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 299 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 300 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 301 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 302 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 325 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 328 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 337 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 338 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 339 nucleotides
<223>  "n" refers to an undetermined base

<400>  33
gtagggcgcc gccgtgacag attagtccta aagggaacgg ggttgttagt tcaattggct    60

accggaaaaa accaggctgg gctgggcgcc cgccatgaca accgataccg gaaaaggcgg   120

gtcgttcccc ccggacagcc ctacgccggc aaaggtctcg agatgtgagt agtgagagcg   180

cctaccccat acngtcggcc ggctcccctt cttttaccca gtgatctaga cctagtctag   240

gacctcggga actaggacca gcctccctcc ttcttggaga tctgaccctc aggattcann   300
```

nnctttgctc acgagctcca acccnacnca tccaaannnc aa   342

```
<210>   34
<211>   370
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 325 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 343 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 361 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 368 nucleotides
<223>   "n" refers to an undetermined base

<400>   34
```

cattgtttac tttcgtctaa acgcggtgga agcccatgga agaaagcggt tagcagcaag   60

gcagagccct gctccctctg cagccccagc tcccagcgcc ctgggctttc caggcacctg   120

tccgggtagg ggattgaggg ccgtggccag gcccgcactt tcctgctagc cgcagctggc   180

cacatgccca tctgaccctc cgagttctcc tctaaaaatg gggctgacag ccgctacctc   240

acaaagtcca caccgggctc aacccgntgc cttcctcccc aacaggactc tgccaccctc   300

cctcaggatg cctgagggcc ccganctgca cctggccagc cantttgtga atgaggcctg   360

ngggcgntt   370

```
<210>   35
<211>   213
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 8 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
```

<222> position is 10 nucleotides
<223> "n" refers to an undetermined base

<400> 35
aaaatacnan taaagcgatg cttcgaattt ttaaaacgga atctctgcac ccaaatgcag   60

gactggtgac ttaaggagct gcgaagtctg atttaccggc ctactctcga cctgcccccc   120

accccagct cagggacct tttgtctgaa cgccagagct actgaccagg tcggggggcc   180

gcggcccaag ccgaattctg cagatatcca tca   213

<210> 36
<211> 173
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 4 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 5 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 100 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 109 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 123 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 144 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 156 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 160 nucleotides
<223> "n" refers to an undetermined base

```
<220>
<221>  unsure
<222>  position is 162 nucleotides
<223>  "n" refers to an undetermined base

<400>  36
gacnncgggt ttgtgtgtaa cagggtcagt ccccgtatct actttgcgaa agcttcgagg      60

cgagcgtgaa gtcaagggct gcggtggatg ggggtaaaan gcctcctcnt cccactgcct     120

gcnccgtctt ggggtaaccc ctanccccca cccggngttn cnctttaatg ctc           173


<210>  37
<211>  369
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 22 nucleotides
<223>  "n" refers to an undetermined base

<400>  37
tcactgtgcc gggtctctcc tncccggtcc aactcccttc cttgtcctca tctctgtccc      60

caaggtccgt gacccgcgga ggtgatgggg gggataggag agccccaggg accgcagagg     120

tgacacaatc gcccgcccgt cctccctcgc tgggagccga ttcagcctgt gccgagcctc     180

tcccttcgcg tgcctctgcg cacagcggtg gcaccgcagg actccgggtc ccccccggct     240

ctccatcggg aagccggcaa atgcgcttcc tcagccagac cgcggcgggg tggggcgggg     300

ggggcggaa gttgaaatac tgggacagaa acacctgccc gtcccaaggg acggaaaact     360

ggatgccaa                                                            369


<210>  38
<211>  123
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 20 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 29 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
```

<222> position is 41 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 87 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 108 nucleotides
<223> "n" refers to an undetermined base

<400> 38
gtcccttcgc cccgctttn ctttccccna ggtcccagcg nccgaaccgg cggatgtcca   60

cgaaacatag ggcgagccgg gggccangcg gggccgtgta aaatctcntg tggtcatttt   120

gtg   123

<210> 39
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 32 nucleotides
<223> "n" refers to an undetermined base

<400> 39
ctagccctgg aagagaatcc gaggctcagc cntgctgcag cacccaggac actgcatccc   60

agcacctgcc cgaagatcag cccaggaccc aaaggaaagc aggctccaag ctccccggaa   120

gccaaggaaa ataggaaaac atatcctgcc ccggggacac cttctggaac tatgaccaca   180

tgcacttgac cttccggaac aatcaccgca tgcacctgac ctcccggaac tgtcaccacc   240

gcgcgcacct gacctcccgg cactgtcacg accgcgcgca cctgacctcc cggcactgtc   300

atcaccgcgc gcacctcacc tcccggaact gtcaccaccg cgcgcacctg acctcccggc   360

actgtcacga ccgcgcgcac ctgacctccc ggaactgtca tcaccaggcg cacctgaccc   420

cccggcactg tcacgaccgc gcgcacctca   450

<210> 40
<211> 593.
<212> DNA
<213> Homo sapiens

<400> 40
ggaccaagct gggtaaactg ccgacagctc cattgggcag catgtccacc cctgatgacc   60

aaatcccacc aaacgtgcag ctggcactcg gccgcctttg tttccttccc ctagaataaa   120

actccgctgc tttcccacgt tcctggagca gcagccggaa taaagcgccc atggccttgc   180

cctttgagtc tcggaggatg tttgccactc caacaatgga cttttaaata attcaggggt   240

caaaaggcgt gtgtgtgggg ggggagaaaa gttacaaatc agcacttgaa accgaacaca   300

aacaaaaatc aaacaaatcc gaactaatat aacaaatcaa aactttgatc tttagaagaa   360

aacttcaacc ttaatgcttc caggaggaaa gcagaaagga taatgactga attgtgaaaa   420

cgagccaaaa tgttccacca ctgatgtcac acacacctat gactccctgc acagatccac   480

ggtcccgggc gctgaatccc cgcaaccctc tgcgcccaca gaggttaaac tctcgctgct   540

ggcgacttcc gcttcctggc ctaaatctga cacgcacgac tcccccgcg gca   593

<210>   41
<211>   457
<212>   DNA
<213>   Homo sapiens

<400>   41
accaccaacc aaatagggcc tttcctgtta acgaccacgc ggcaagggggg ccgggccctc   60

gcacgcctcg acggcctccc ccactccaaa gggactccga tttcgcagga tctcccgcct   120

cccgcctctg ctcccaacac cctacgtttt tctcttcctc ctcatttacg tatttacaat   180

aaaacagcga agctgcacag tctgtctcta aatcaaacgc ggttaccatc aaagcctcag   240

actctatgtc tcaaccgcaa aaggtctgac aggaaatcaa ctcgggagtt tgtcaattct   300

ttaaactcaa agctctgtta acgaaatctg gatctttcct cgctccccac ctgcctcccc   360

tgacaggaga atgactgtaa aaggatcctg tcgtccccga aagtcagcac caagcacttc   420

acaaattgtc aaatctcaaa agcttacacg cgcggca   457

<210>   42
<211>   211
<212>   DNA
<213>   Homo sapiens

<400>   42
gcctgacctg aatgacgcgc atgttgaggc cggtctcctg cgccagctgc tcgcggatgt   60

ggcgggtggg cttgggtgta gcagcgaagg cggccttcag cgtctccagc tgcttggctt   120

tgatggtggt gcgcggtccc cgccgcttgg cgcccaggtt ctggtcgtca ttctcgttgc   180

tacccgcttc cttgtccgac acgtcggcgc a   211

<210>   43
<211>   141
<212>   DNA
<213>   Homo sapiens

<400>   43
aaatcatctc cggggcccca gcacggacac gctccagacc cgtgagttcc ccagcgccgt   60

gccgggaggt caggggcgct gaaagaagga agaattcagc cacctctcag catccctgtt   120

acctcgagga cgcgcctctc a   141

<210>   44
<211>   559
<212>   DNA
<213>   Homo sapiens

<400>   44
acccactttc cattaacact aaataaaacg catccatgga tttcctctcc attccgaggc   60

aacaggagtg catggcacat tgccctactc ccctgaagct cttcgctaac ctaagactcc   120

agggtgagga agttagctgg agctttttaa agtgcatctc caaagagaat tttgctcaca   180

ccatgagagc ccccaagaaa caccagggcc cccttagatg ccggagacca cgccctccag   240

gaataagccg caccctctgc ccagcagatc cttgcgcgag tagccctctt tccctggggc   300

taatcaagtg catgccacat gtcaccactc tcagctggca attcttcctc agaggcgcag   360

actttcacgg aatccccagc aggggggggtt aagagattca ggggaggccc cgcccgtgcc   420

ttccacaaaa gtcgctttac cgtggctcgt gtcctgcggc cccaaggggg tagcctggga   480

cgtgtattgg gagggcatag aggctccttc caggacaagc tgccagcctc cagtgggcaa   540

ccatgtgaga ggcaaaatt   559

<210>   45
<211>   433
<212>   DNA
<213>   Homo sapiens

<400>   45
gcgaacagca caaaggcttc attcctacga gagattaagt tttagagcaa atggacacga   60

tcgttaaaga atttgatatt tccatgtaaa ctgcattagc aggttatgcg atccaaactc   120

acaggaacaa ctccaactct cggccatgcc ctatttcatg tctagatttg tttaaccgac   180

ttacatcata atccaagaat acgaactaca gtatattctt acagcaaagt tattccttaa   240

aagcaaaacc gagccacctt tgaaaacacg cacacacatt atccacggca ctaaaacccc   300

agtcttgacc gagaaagacc aacaacttgg gggggaagaa aacaacttca gagccagagc   360

```
tcccaaagca gaaagcgctg gcggctgaag ggcacacgag gttccgctcc cgggcgaacg      420

ggcggcgtcg caa                                                        433
```

<210> 46
<211> 487
<212> DNA
<213> Homo sapiens

<400> 46
```
cccttagtat tccatgagcc accattttcc ccacgatccc tccagcctga acgatcacat       60

cctactgtgg accacgactc tcccagcagc gggcgtttaa tatccagtta gcaggttctc      120

accacccct cgctggctcg aatacagcat ctgcaccgag ttcccgagaa tcgtcaaccc      180

agcaaatccc ttaattggtg gacatgaaaa tccagggctt tgtgctgtaa taacagagtc      240

ctgggggcct ggggagtttg tgccgcttgg agctcaggtt tctgggacag aggctgagcg      300

cagggcaggg aggcaggtct cacctggcac ctcccagagt cctcgccgag cagatggaag      360

cagaggctct cgcgcccggc ccccgccggg agacctctct ctctttccct cggcctgctc      420

tgccctctcc cgccttctcc ctgtctgatc cttctctgct gtcatgttct ttgtcctcgc      480

gccccga                                                              487
```

<210> 47
<211> 403
<212> DNA
<213> Homo sapiens

<400> 47
```
gtcatataag cacaaccatt cccagggcca ccctggatgc atcagatcag tccccccact       60

ggtgaccaca atggctggct cagagtgcct ttgaacagac aggagaaaca gacttcttgg      120

agggagggac cttcccacag ggaatggcca aggagctagg tcttcagggc ttgcatggcg      180

tggagtgtgt gctcaggtgc acagtgaagc aaacctgagg ggacttgggc cctgcgtcct      240

ccagcacaca cgcacccttt cgccgtcaca tccggggcac ccacccgtgg aatatgtgag      300

ccgcacttgg ccagccacga gttccagggc caggaagtcg tgcttctcgt tcaggcgccc      360

gttgtagaag agcagcccgc tctgctgcac tgtcgcgtcc cga                       403
```

<210> 48
<211> 155
<212> DNA
<213> Homo sapiens

```
<400>  48
ggcgtggaga ggaggggggca gaaactcagc cgcccctacg tttgctaaac tgcgtccgcc        60

aggggggcgta ttttctaaa acgcacaaga cgtttcgtgg gttatcgatg gtctcttgag        120

cctccttgac tgatgggggat tgaccgggcg ggata                                   155


<210>  49
<211>  256
<212>  DNA
<213>  Homo sapiens

<400>  49
tctactgagc ttttctttaa gtggaaccag aagtgctggg atgagaggga aaggatggga        60

gtgcgtccaa aggtggacag caggtcccca tccctggtgg gagtgagact ggacggcatc        120

ccccggaaag gtggtttggg ccttggacaa ggctagaggc aggagtccat gatgcagaga        180

tgacacagtg cccctccgcg tgtgagtcca cgaaggtcac tactgaggct ttgtgcttgt        240

aaaaggccgc cccgca                                                        256


<210>  50
<211>  224
<212>  DNA
<213>  Homo sapiens

<400>  50
tgcggggtcg tgggggaacc ggcgggagct gttcgctggc cggcctcact ggagtaggaa        60

ttttagatga aactgagtcc gtttctcctt gaaggcaggc agtattctta gatctactat        120

tcatttaaaa agaaggaaaa gaaaaaaaaa tgactgctac ttactgagaa gaaaatttct        180

gttctcctcc gattccgctg atcccgcttt atccgcgcac ctca                        224


<210>  51
<211>  313
<212>  DNA
<213>  Homo sapiens

<400>  51
gtggctggga cggcccaggc cgcggcttcc cgcgtgggga tgcgctgtgg cgcagagctg        60

gtcccggcgg ggccaggcgt ttgtgggcgg gtgacgggga tctagggctt ccgctcgtga        120

ttcctcttgg gctgtctttc cgggtttgga ctcgcctgcc cggctgtgtg cagggttccc        180

gctgcctctg gccggcaggc gtccgggctg caggtgggcc ggcaggcagg tgttagcggg        240

aagggagcac aggtagcgag gtgggatcgg cgacctggct agggtgtcgg cagaatggaa        300

tgcgcggccg cta                                                          313
```

```
<210>   52
<211>   385
<212>   DNA
<213>   Homo sapiens

<400>   52
tacgttgcgc attcattctg ccgacaccct agccggtcgc cgatgccacc tcgctacctg        60

tgctcccttc ccgctaacac ctgcctgccg gcccacctgc agcccggacg cctgccggcc       120

agaggcagcg ggaaccctgc acacagccgg gcaggcgagt ccaaacccgg aaagacagcc       180

caagaggaat cacgagcgga agccctagat ccccgtcacc cgcccacaaa cgcctggccc       240

cgccgggacc agctctgcgc cacagcgcat ccccacgcgg gaagccgcgg cctgggccgt       300

cccagccaca cccagcgcgc cttctccagg gtcagccagc tgcggctctg ccgaagcgct       360

cctccgctcc tttctcgcgc cccga                                            385


<210>   53
<211>   307
<212>   DNA
<213>   Homo sapiens

<400>   53
aacccggctc ggttcggcaa ggttcaggga gacaaggtag agaaggctgg ggtgagcaag        60

aagtcgggcg gccgatcgtc agggccacga gcctcgcctt gccttcttgg aatcccaccc       120

aactttaaag gcccaaagat cctgaaaatt ccgaaagcga aactgcgggc tggtctccag       180

aagtttgaga acggtctccc aggctttcca gcgtcgtccc gggattctcg acaccacaa        240

acgccatcaa ccacgagcac cggtgtccgt ggctattgcc ccgaatggtc cccatccgcg       300

tccccta                                                                307


<210>   54
<211>   182
<212>   DNA
<213>   Homo sapiens

<400>   54
cgatgtcgaa gccgtttgga gggaacagcg gtttccaagt tcctgctgac ttgagaagcc        60

tctgcgggtt tccgaatctc cggcgcactc ctgggcgcgc tgcgggagct gtagctcagc       120

cagccaggga gtagcggctt tcatccgccg ggaggagtct ttcgagttca atcgcggggg       180

ca                                                                     182
```

```
<210>  55
<211>  523
<212>  DNA
<213>  Homo sapiens

<400>  55
tcgggtttga tccgccccaa ccaaataggg cctttcctgt taacgaccac gcggcaaggg       60

ggccgggccc tcgcacgcct cgacggcctc ccccactcca aagggactcc gatttcgcag      120

gatctcccgc ctcccgcctc tgctcccaac accctacgtt tttctcttcc tcctcattta      180

cgtatttaca ataaaacagc gaagctgcac agtctgtctc taaatcaaac gcggttacca      240

tcaaagcctc agactctatg tctcaaccgc aaaaggtctg acaggaaatc aactcgggag      300

tttgtcaatt ctttaaactc aaagctctgt taacgaaatc tggatccttc ctcgctcccc      360

acctgcctcc cctgacagga gaatgactgt aaaaggatcc tgtcgtcccc gaaagtcagc      420

accaagcact tcacaaattg tcaaatctca aaagcttaca cgcgcgggca ctccggaaag      480

gctgtgggga ccacccaaag cacccccctc cacaccgcgg gca                       523
```

```
<210>  56
<211>  795
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 741 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 762 nucleotides
<223>  "n" refers to an undetermined base

<400>  56
tttactttct tccggctgac gtccatctcc tcaaatttct caggaatgtg gggaagctcc       60

tagccctgcc tgcctttcta gagggcttct tggatttgca gcttctaaca agttgctctc      120

gccacggaga agctgttatt atgacaaaat atttggggca ttatcaaaat cacacaggct      180

gctgggctgc tgtcggtttc tcgccagggc cagtaagcag ttacatttgg agttgctacg      240

tgttgtttgg gggccgggct gtggagagtg actgagccag tattttttcat ccaaaattct     300

gcaaattgaa ttaaccacaa ttctagtctc acctcccgtc tttaaaaaaa taagttgaag      360

aaaaggtaaa tattagagat aaggcagcat ctagtgactg cggagaggca caagctggtg      420

ggcgagggtt gggggagtca gcaaagccct tcaaaacctc cccgtttaat tttctggctg      480
```

```
tctctgcatc ctgttgccag aattccaaat gcttggagtc atttanaggt gcgagaactc      540

aaacgtcgtt ccacttggaa aggggaccgt ttaacgttaa attccattag cacctaaatt      600

gtttcttaaa gacatccgct cagacacagg actcgaaagc gagcatttca tgcaaataaa      660

tttctcaaat tttaaacctt gttaaaagct tgtctcgcac ctcggctccc tcccttccc       720

cggaaganaa caataggccg ntggcgcatc cccacttcgg antaaatatt gacgggggaa      780

gttgctaaaa acatc                                                       795
```

```
<210>  57
<211>  438
<212>  DNA
<213>  Homo sapiens

<400>  57
gcctgtgtgt aggggactgg aggtggggga acctgttctt ttcttgtgtc tgatcctggg       60

gctcgcttcc tgggtcctag aacagcagcc aggacggaag aaactgttca cgttgcaccc      120

ctttctctaa gattcccagg ccaagagtag ctgcagaagg tggccctgaa tctatggcct      180

ccttctctct gcctgacccg gctagtggat ccggagaggg gaccagggag agctcctccg      240

agcaggggtc cttcgggaga cagagagggg tccaggctga gagaactctt caagcatggc      300

gagtctgcgt tatagaatcg ggcgggcggc tcaacttggg ggaagcacca agaagagctg      360

ggcgacctgg agcgcagaac cggctttggg gagccacccg gcggggcagg ggtagcacgg      420

agcccgggcc gcggccca                                                    438
```

```
<210>  58
<211>  611
<212>  DNA
<213>  Homo sapiens

<400>  58
gcttcccct tcctttctcc cgcgctgccc ccttgagatc cgacccttcg tgtgtttgcg       60

ctaaattgtc ctcgctgttc ctctcacccg cgacatacag agaaagtaac cggagagccc      120

tacatatgcc agtctggctg ctgccctgga gtttgcatcg atcctgcaat tcctagtcaa      180

atatgaacac tcctctccct cctcacgccg agttgaaaaa cgtgataata atataagtcg      240

acaggctgta ggcaatattt ttcactgcat gacttattca tggcgaaaat gtaaactgtt      300

ttcccacggg ctttattaga atgttgcctt ctgccgagat aggcttcacg caagccctgt      360

gctctcagtt tctctggcgt gagcaaaact gtttgggtcc ataagtgtcc acatttggcc      420
```

```
atttattatt tcgatttgaa ttttcagtaa atacaaccac cccttttcccc tcccccagaa          480

acagtcatgc ttagagaaaa ttatagcaaa acctccctgg aagcctgaag gttttggatg          540

actgagaggt ttggtttggt ttctctttct tttcattcaa aacggatcaa actccctggc          600

tcgcgtcccc a                                                               611
```

```
<210>    59
<211>    291
<212>    DNA
<213>    Homo sapiens

<400>    59
gagtttggca ggccccggat tccacaaagg agtaggcgcg gccagccgcc tccagccctg           60

agctcagtaa attcggtgtc ctgaatgctc ccttcctgtc cttaccactg cgagctctct          120

tgggacagct ttctaggttc cactgcgacc tactttccgc tccctgagtg cttctttgct          180

gaaactgcag gcgaaaagat ctctttccca gaccgcagcg cactttgaga aggggctcaa          240

agtcgcccgc tctgaatccg gcaccggcaa ataggagtag ccgcatgcgc a                   291
```

```
<210>    60
<211>    226
<212>    DNA
<213>    Homo sapiens

<400>    60
gaaaacagat aaaacgccct acagaaaatc tcggcgaagt cccggaggac tctggtttct           60

aagatcagct gggcgcactt tctccgggac gtcccttctt ctcggtctca gcgccttcct          120

gccctcagcc gcgcgcagct ttgttttggt gacaaactga aataagaaat ggaaatatat          180

tggcctttgc tgctgccagg gatgagaggt tgttgacgtc ggcgca                         226
```

```
<210>    61
<211>    580
<212>    DNA
<213>    Homo sapiens

<400>    61
ctgtgatgca ctcggcggat ctcggtggca gctgcctcct tcatctccag tgacgcctgc           60

atgctgtcct aggcagtgtg aggagtgaag atgagatttg gcgcatcttt caacggagtc          120

tgagcaaagc taaagggctc cgattcgtgc aagccaaggg ctgcccctcc tatcctgtcc          180

tccttgagga cctgtgctaa ggctttctca tccaccaggc caccatgggc tgcgttcaca          240

aggaatgctc cctgtctcat ctgctttata gtaaagtcat tgacgaggtg gtggttatgt          300
```

36

```
tcattgagat tgctgtgcaa cgagacacag tcactctgat acagcaaacc ctgcagggtg      360

tatcagggtc ccctctgcat gccctgggac ctctctatct tgtcctacaa gtaggggtca      420

taaaatacga cgctgaatcc aaaggccttg gctcaaactg caaccgcctg cctcatgcaa      480

ccgaagccca tgaggcctag cgtcttccac gaatgagggc cactcccatg gccacctcga      540

gaatctgctc cacgctctga acccgcgcac ctcaagccga                            580
```

```
<210>    62
<211>    633
<212>    DNA
<213>    Homo sapiens

<400>    62
gcccaggaga agccctccac ggtgggcgtc ctcctagaca accagcaccc cctgcaggca       60

ccctcgtctg gcagaatcag ccctttccca cctgcaggcc cttctcagcg cctctgactt      120

cccacacaca gcacaggtta caaactggtc cctggcagtg cactctagcg ggcctctctc      180

acaagttctg cgggcctcgt ttcatggaaa gcgggttgtg gattcctgct gcccttggat      240

ggcccctgcg cacgcacacc tctgagcggg cactgagcga gcgtggggag ctgctccctg      300

ggaactaggc aggagctttt aaacaccctt acacacagcc attctgcggg aatacatgct      360

ttcccggtaa ggctttact gttcattcca ggtaaattgg aagtcgcaca ccccaagctc      420

caaatacaac tcgttagctg gcaggtctct gaagccaatt ccttctgagg aaaatggaga      480

taatagcagc taccctccca ggtgactggg ggagaataaa gtggctgtgc atagtggtgt      540

ttgcagctgg tggctgctat tatccttcat tacagcttgt aaaaagggtg tctaggccat      600

ttacacacag ataggccggg tggggtaagc cga                                   633
```

```
<210>    63
<211>    703
<212>    DNA
<213>    Homo sapiens

<400>    63
gcctatgaat ggatttataa ttgctttatt tttgtcccat ttagacagaa gtcagagaca       60

gaggagagaa ccaaaaaact tggatgtttc cgtaaactag attcgtcaat cctcgataat      120

tgaaagtagt tccagtatgt cagccaccgg ggttccctgg ggagctaacc agtcctgaag      180

gaagtatgaa gaggaagagg aggtcttcag ttaaggggat gaatttgtgc agtcctaagc      240

cctgcaaagg tgctggaggg aggaagaagg gcaggaaata aagatggaa gaaaatttgt      300

tttttatcca cttagagttt tatctttaat gatgggaaac agtgctgctc tcaggaaact      360
```

37

```
cagtgtggag atctaggagt tcacggttca tagtccatta ggagcaggaa aaggatagag     420

gacatttata aagtaacatc caagtccaaa gtaaaatggt ataaattgtt tcccatgata     480

aaggctggct gagtaggtca ggaaaggtct tgtcagacca tatgtgctgt ttcaggctgc     540

ttcaaattct tttaggacag tggtggatat gagtgaagac ggggcaggca ggccacatct     600

cttagaagag gaaggtgatt gccacgtctc cttcctccat gctgatggca aggcgtgcgg     660

gctgtgttct cttgcagcca gcgtcccatg ctcggcggcc aaa                      703
```

```
<210>   64
<211>   420
<212>   DNA
<213>   Homo sapiens

<400>   64
gtgacgtgcg gaatacacgt gatgtcgggg acaggagcgg gctgaagagg gcacgatccc      60

acgcggaggc cacccctcac ccggggtagg agcccgctgc acttgctgtc gctcagcccg     120

ggcgctgcac cacggcagcc gccatgctgc ttaaagccgg tcatgtgacg cgggagccag     180

ggtggaaggg gtccccgcgg gcaagccttc gacacgtgac ctgccacccg actacggaag     240

cctcttgggc gttccgcccg ggctcacatg tcatgtgacg gccggccggt cgccggagta     300

accaggaact ttcccagacc ctgcggtccc tggagcgtca aaaagagcgt ccccgtgact     360

aggtggagtc gcctgccctt ccgaatctca gctgtcttat ctggaacccc cacgcggcaa     420
```

```
<210>   65
<211>   496
<212>   DNA
<213>   Homo sapiens

<400>   65
gcgctgcacc aatttagagg gtagaaaaag gagttagaag caaagaggaa aaaataaata      60

aacaggcaac aaaaacccaa cccagccagc ctgagccatt tgcattagtg ttcatttagg     120

aaattagcag acgggaaacg ctggggagtg gagtgggccc cggccttggg gactgcagag     180

cccgctcagc cctgggtggc tgggcccaca tggctgtcgc caggagcaca ggaggaccca     240

gaggtggccg agggagcctc gccgggctcc ggtatgggtc ctggcccctc acaggtgcga     300

gcctggccca gtgactgtgg acgctgtggg agagcaggcc tccgatacgc agggctggga     360

ctgctgacct ggaaggtggt gccgggcgtg tctggtgaag gcgccgttgg cagctagaga     420

gagacggcgg atggggtgac gccataaccc acgtcccag ttttgaggct tgacggtgac     480
```

38

```
ggaaaaggac gtcggc                                                        496
```

```
<210>    66
<211>    637
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 612 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 627 nucleotides
<223>    "n" refers to an undetermined base

<400>    66
cgccgagccg ggatgagcaa ggcttcctgg aggagagggc cggcctgagc ttggaaggat      60

ggggaggagc cactggctac aagggtgtag aggtgagaac cagtgtgacc tgcccatcgc     120

tggtcgtctc tgggtcattc agctgaaatg gcatctctga gctgagagga gtgttgcctg     180

taaggagcta ggcatcagcc cccagtagag gggcggccca ggcacagccc atagccgcag     240

acttagtgag tctagctagg gagacagtag aggggccaaa atgaggacac aggtcaccaa     300

aaatcctggc caggtcctgc cactacctgg ctcagcgacc tgccccccccg agcctcagtt     360

tcccccattg gtggaatgga gtgaggaaga cgcgcctccc ggggctgcga tggagaattg     420

agtcagagtc tgggggtgct gggagggctg gggagcagcc tccctgagcc tcagtttccc     480

tggctgggga atgaggacct tgctcgtccc ccctcataag gggaagctgt caggaaagtg     540

ctttcaacgc tgagccattt cccagtggtg cacaattagc tttccagagg attttggtgg     600

attctagagc tngagggctg ggggatnggc ggccaaa                              637
```

```
<210>    67
<211>    595
<212>    DNA
<213>    Homo sapiens

<400>    67
gccctgagct cttgagggcc tctgcagttc ttgggacaat tctgggacta tatctttggg      60

ccttggtgag atctagaggc tctaaagtct ttgggagggg tcctgagctc cgtggacggc     120

agggtcttgg gcactcactt gcattcttga ggggtgtgtt tggcctcgtc cgtgcaggtg     180

tagaatttcc cctgtagaga ggatgtctgt caagtaggtt cacccttcat cacactcccg     240

cccagacccc tgcctggcat tccctccagt gtttgcccca ccttgaagag ctgcaccccg     300
```

```
atgcaggcga acataaattg cagaagtgtg gtgacaatca tgatgtttcc gatggtccgg     360

atggccacaa atacacactg caccacatgc tgcgggcacc caagcatatg gctactgaac     420

actacaggcc acagtggtca tggggcaggg actctggtca tagatgcagc tgagggactt     480

gggctgggga catgtggtga tgggtcaggg atgtatggtt agcaacatgt gttcaagagg     540

cagtgttatg ggctagagac gtgtgggcat ccaccaggaa taagtgtttg ccggg          595
```

```
<210>    68
<211>    580
<212>    DNA
<213>    Homo sapiens

<400>    68
gagtcaggac ggaggacgcg gcaggtcaca gagcccacca agtccgaagc tggaagttca      60

gattctttga tattcaaagg tggatcatct gtgctttttt tttttttatca gtctctcact     120

ttttatccat catctaattg tgacagctta tttgccttta taccataaga tggggagtag     180

ggttgagatg aaatccaagc atcgtttccc ttccccgatg gtcgcctccc tggggtgaga     240

cgttcgacgt gtcagacttc accaagagca tctcccgcct cggtgcagta atgaacttgg     300

aaacgattta ctccggcact tggttcctgt ctccataaat gcggctgctt taaagggaat     360

gtaaaaaggg ctgtaaattg gtattgattg ccggtggtct tgaagaaccc caactgagga     420

ttgaccgttc cttggagtga aggctccgca ttcagacgcc tttcgcctta cgtcatcata     480

attgagaagg gaaaggagac gtgttagttt cagtctgatt atttaccatc aaggcataaa     540

cacttctcag aggcagcgga acccattaaa ccggcccgta                            580
```

```
<210>    69
<211>    589
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 559 nucleotides
<223>    "n" refers to an undetermined base

<400>    69
acacggggggg caacctcttg cacctggctc cctgccctcg gtgccacgtt tccagggttc      60

ctccacgtcg caggctgtgt cagcctcgct ccttccactg cagaattgcg gtccacagcc     120

tggatgggcc actctccatg tatccacctg tccctccgtg gctgctgggc tgagtcgctt     180

ctgatgctaa caagaggcgt ccggctggac taaggccccg gaagctgaga actggagggc     240
```

```
aggtgcgggc atcgggcaga gcagctccag caggcaggac ctggggcctc caccctgcac          300

ccctgtgccc cgcgtgtggc ggaaccgccc cgaggggagg ctgtcaccac ggtgacaggc          360

agccccacgc gagcctgaga accctcagcc cacctttttc tgtaatcaca gcaggcatct          420

ctccggcaag tcaatccagt tccagctggt gctgcctccc ttgcctcatg ggctttattt          480

tagaactctg agcaataata aaaaagacgc tacccgctac aatagatgtg gcagagaatc          540

tggctcttca cttcatcana gatcaccctg aaatgatggt tgttgttaa                      589
```

```
<210>    70
<211>    748
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 10 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 412 nucleotides
<223>    "n" refers to an undetermined base

<400>    70
gctacatctn ctctacattc taactaacac ttgttatttt ctgtttttgt ttgtttgttt           60

ttaatagcca ttctagtagg catgaagtgg tgtttgcctg cttttttttga tggaggtgga         120

ggaatagggt ggaattggtc cttaaccatc aattaagctg ggggccttag acctctgtga          180

attggctgtg acaatagcta aaggaggctg ctacctcata ctgaagagat gtttcctaag          240

tttgtcaccg gagagggcac cgaaccaact tattgtcttg gagggaagaa gcagcaaggc          300

agaagacttg aacttctcag agaaaaaaac agtctacaga cttcatttta tgctgtcctc          360

acacactact gaaagctcta ccctggggac ctggcttgac ttctaaccta cncctgtgtt          420

atttaggaag agctcccagc tgctctgagt ctcagtctcc caatcagtga aatggaggca          480

atagcacctg cctggctgca tcgccccaca gtgctgcaat gagcatccaa cgagagaaag          540

cttgtcacct gtgttgcaaa ctaagttaca caaatgcagg cagtagcagc tagaagaaaa          600

tggttgggaa tctgaaaaga attaaagccc cccatgaatt tcttctcacg cctcctccaa          660

aagccaggga ctgcttcacc ccgcctccag gactgctcgc tccagcattt ccggcagctg          720

ctgacagaat gtatgttgcg gctgtccc                                             748
```

```
<210>  71
<211>  599
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 491 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 522 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 538 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 584 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 596 nucleotides
<223>  "n" refers to an undetermined base

<400>  71
gatgactgtt gcccgagctg aggccacgac ccaaccccga ggaagggaga acagcttccc    60

atgaagggca tggctgctgc cccataatcc cagggcagga aataaaggga tcttggacta   120

ggcaatcaaa ggacttcctc tccctctaag gccaaggagg aaatgtggct gggactccaa   180

gctctgtgga tgcctggagg tgccagcagc tggggatcag ctggccccac ctgcagagcc   240

agccagtggt cccccctgcat ctccaaggtt gggtctatgg gctccaagaa caggtgtttc   300

tcagggtaac ctcagcccct acaacttcaa ccaagagagt gaaggggagc agccctggag   360

gccaatgagg aggggggatta gtggtcactg atgacaaaga catccctgtc cccagagcca   420

gccccttgtg agcagaagaa tggctgccgg gcaaaaggac ctgctatgcc ctccccatac   480

acatatcatg ncacctgggg accctctgaa taacaggggg cngctttaga gtggcttnat   540

taccaacaag aggcccagaa gggctagagc acacgatttc atgntcggcc gcatgncaa    599

<210>  72
<211>  614
<212>  DNA
<213>  Homo sapiens
```

<400> 72
gtgcgctatc acgactgttg cccgagctga ggccagaccc aaccccgagg aagggagaac   60

agcttcccat gaagggcatg gctgctgcca ccataatccc agggcaggaa ataaagggat   120

cttggactag gcaatcaaag gacttcctct ccctctaagg ccaaggagga aatgtggctg   180

ggactccaag ctctgtggat gcctggaggt gccagcagct ggggatcagc tggccccacc   240

tgcagagccc agccagtggc tccccctgca tctccaaggt tgggtctatg ggctccaaga   300

acaggtgttt ctcagggtaa cctcagcccc tacaacttca accaagagag tgaaggggag   360

cagccctgga ggccaatgag gagggggatt agtggtcact gatgacaaag acatccctgt   420

ccccagagcc agccccttgt gagcagaaga atggctgccg gggcaaaagg acctgctatg   480

ccctccccat acacatatca tggcagctgg ggagccctct gaataacagg gggcgcttta   540

gagtggcttc attaccaaca agaggcccag aaggggctag agccacacga tttcatggtc   600

ggccgcatgc gcaa   614

<210> 73
<211> 552
<212> DNA
<213> Homo sapiens

<400> 73
aagcgcccac agatggccaa gcatgtggag gagagcacaa tattttattt aaatatccaa   60

atacgaacac attcccgcat ggcaccaaca gccgcctgaa cacgcccgat gccggcttgt   120

gcttttttccg ttttgtctag aaatttgggt tgcactaaat tctcagctga atgaagatga   180

gaaggggctg gcagaggggg tggctccagc tctctgagaa cctggctcct tcccgggtgg   240

cagggagaga tggcccctgg ggagacgggg agggtgcact gcctcatgcc caaaccacca   300

gcttctagtt gagaaatcag aattttctct gcagaataag gaaaaagcat tgtcaccatg   360

attcacgtgg agctggccac actcaggaaa ttcaatgggg tcccacaggg gctccgaggg   420

ggaaggagag ggcctgggac atgcccctcc agccatcatg gaacaggatg ggcagggccg   480

gccctcactg ctctctaaca gtgaaaagcc acatctccac tttggaaaac acaggcatgt   540

gagagcctgg gg   552

<210> 74
<211> 450
<212> DNA
<213> Homo sapiens

<220>

43

<221> unsure
<222> position is 378 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 403 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 409 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 440 nucleotides
<223> "n" refers to an undetermined base

<400> 74
tggaggcttc gagggaagtg aggttccctc ggacaccota gtgggaaggc tccacgcggt   60

aatggaacca cgctgtgaaa cctttgcctt tgggtgtcat ggtggaagca aatcttagaa   120

gacatttaat ttaaaaaatt cagttttaaa aaatgttgac ttaaaaagca gttttgaaaa   180

acaacctgga attagcctga gatcgatgcc aactcttagc agtctgtata ctaaacacag   240

ttaaacaact gtagctgctg gcaagctgga acctttttgt aaagaagcac ataaaaagga   300

cagaactggt ggaaggtgca ctggtctttc cacatcgcca ccaggcgttt tgaagcgtgc   360

tgctgacacg ctactcanat gcttctggaa gccaaacaat aanaaaaanc cccattgttt   420

cccttgctgg gttttacccn ccatggtgga   450

<210> 75
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 417 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 421 nucleotides
<223> "n" refers to an undetermined base

<400> 75
ggacaatgag gagggggtgc acgtggaatc cccacggata ggccggacgc cgggcaggag   60

cctttgcagg ggtgcacagc ctcctctgga agccctggtc gctgcctggt gcctgctgca   120

```
ccctgcgggc tccgcagcgg tggagccagg cctgaactgc ctgctcttgg ccccgcctgc      180

ggccctctgc cctttgtctt gcccgtgggg cccggggcct caagctggcc cggggttcct      240

gaagttagct gacgatgggc tggcctctgg ggctgggtcg tgggccttgt gcactggccg      300

ccacgtcacc agcgccaggc ctacccgcgg tgctgctgga gacgcgggat gcccgggctc      360

gggctgtgct ggatcccctg gcgctgcgaa ccccgtaccc ctttccaatc gcgggcncgg      420

nttaaagccc ga                                                         432
```


```
<210>  76
<211>  501
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 18 nucleotides
<223>  "n" refers to an undetermined base

<400>  76
gacgagacct agccggcncc atgcgcgcct tgagcctggc gaacagttcg gctggcgcga       60

cgcgcctgat gctcttcgtc cagatcatcc tgatcgacta gaccggcttc catccgagta      120

cgtgctcgct cgatgcgatg tttcgcttgg tggcgaatgg gcaggtagcc ggatcaagcg      180

tatcgagccg cccgattgca tcagccatga tggatacttt ctcggcagga gcaaggtggg      240

atgacaggag atcctgcccc ggcacttcgc ccaatagcag ccagtccctt cccgcttcag      300

tgacaacgtc gagcacagct gcccaaggaa cgcccgtcgt ggccagccac gatagccgcg      360

ctgcctcgtc ctgcagttca ttcagggcac cggacaggtc ggtcttgaca aaaagaaccg      420

ggcgcccctg ccgttgacag ccggaacacg gcggcatcag agcagccgat tgtctcgttg      480

tgcccagtca tagccgaatt c                                                501
```


```
<210>  77
<211>  826
<212>  DNA
<213>  Homo sapiens

<400>  77
gcgccctgtg gggatgacgc accatcctgt ttgtttgcac caagtcattt atctcgtgca       60

ccccaggggg ccgtggtccc tgccgggcca tcatgtctgc ttcccttatt tgggttttct      120

gccccctcac ttcatttctc acttcgcttt tcctccttat ccctttgcag tcttgctttt      180

gggggcattg ctcagccagt aatttgaggg acacctcgtg gagccctagt gtggagccgt      240
```

```
cagagcctgg gtaggattct ccgtggtgag gtgctcaggg agacacagga gcattccggc.        300

gcctgttcct tgtgcacatc cgcaagtgtc tgcagtgaga ggcatgggtc ccatcttgaa        360

tgccaacaat gtggcaccca cacccacttt gatggggccg agccacagct ggccaggttg        420

accaccatgg acgtgccaga ggcatccgaa acccagctct gcccagctg ttccactgcc         480

aactccagcg ttagcaaagc agctctccct tgctttgtct ctacagcag agaacagatt         540

aaaagagaag ctgcaggcag agaaatgcct cttggagcca gatgccccaa aggatctctt        600

tgaacaaagg gttgctcagg tcagcgttag ttcctggcat caagcaacaa aatcagagat        660

gctaacagtt ctcagattca ctccaagtga agactcaaag ctggatttat aaatccccac        720

agagccgctg tgcagaggta gagggccggt ttcaggatga ggaagccctc ttggaagcac        780

cgtcctccgg ctaacaagcc tccaacctac tgtcggcagg gagaac                       826
```

```
<210>    78
<211>    433
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 16 nucleotides
<223>    "n" refers to an undetermined base

<400>    78
tgcgcagctc cgcgangtgc ccggcgggcc cgaccctcag actcgcttgt ccctggagac         60

caaccctagc gaccaggctc tgccggatcc cgtcgggttt caactcctat tccgaaggtc        120

ctttctcccc taatcacaac acccactcgc ctcttttttcc tcctcttcct cagcttccac       180

cgccgaccgg gcagccccag ttacccgata acggctccca aggccccgtg tttacattct        240

ttcccactgg aagcagaaat tatcacgccc aaattcctac ctgccttccc tggattcctg        300

gtttcctaag aaacgggttt ggcccacccc tgggcgttcg aacagtccac agaagcgggc        360

aaaggaaaga cgactcagtc tttcccctcc gccaatctct tctccgggac cacagatccc        420

agaagtcacc gcg                                                           433
```

```
<210>    79
<211>    424
<212>    DNA
<213>    Homo sapiens

<400>    79
ggcgggcccg accctcagac tcgcttgtcc ctggagacca accctagcga ccaggctctg         60
```

```
ccggatcccg tcgggtttca actcctattc cgaaggtcct ttctccccta atcacaacac     120

ccactcgcct cttttcctc ctcttcctca gcttccaccg ccgaccgggc agccccagtt     180

acccgataac ggctcccaag gccccgtgtt tacattcttt cccactggaa gcagaaatta     240

tcacgcccaa attcctacct gccttccctg gattcctggt ttcctaagaa acgggtttgg     300

cccacccctg ggcgttcgaa cagtccacag aagcgggcaa aggaaagacg actcagtctt     360

tccctccgc caatctcttc tccgggacca caaatcccag aagtcaccgc ggccgctaag     420

ccga                                                                  424
```

```
<210>   80
<211>   285
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 14 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 27 nucleotides
<223>   "n" refers to an undetermined base


<400>   80
caaccggggg gcanaggcga tcaaaantgg ggtgcgctgt ggtgggcgac acgtgtggcg      60

cgggtctcat tatccgccct tttcacttcc tggactggaa atggcagacc atatgatggc     120

aatgaaccac gggcgcttcc ccgacggcac caatgggctg caccatcacc ctgcccaccg     180

catgggcatg gggcagttcc cgagcccccca tcaccaccag cagcagcagc cccagcacgc     240

cttcaacgcc ctaatgggcg agcacataca ctacggcgcg ggcaa                     285
```

```
<210>   81
<211>   401
<212>   DNA
<213>   Homo sapiens

<400>   81
cagatatgta tcctcctctt tccaaccctg cgtccctttg aggcctggtc ggcgttccca      60

acctgccccct accccaccaa ccctgtccc tttggccatt agtcccggat tatctagcga     120

tgccccgtgt accgtctggc tttgctgttt actccgcgct cggccagttg aggccttttg     180

tatttattcc tgattttctc atagggtaa agtgccttcg ggaggatagg acaagtccca     240
```

```
tcctgttcat acgaattaca gctcggactt ·cgggcccttt tacactgcct tttgtatctg      300

ttaacttgcg ctaaaaacga ttcggttctt tttttttgagg aaggggggttg gggggcggag      360

actctgtcgc ccagtcctga gggccgcggc gcgcaagccg a                           401
```

```
<210>    82
<211>    268
<212>    DNA
<213>    Homo sapiens

<400>    82
atagcgcgca caactgtgtc tcttacccag gcacatgcac tatccctgat cccggtgcat       60

gatgggaatg tagtcctgca gccctgtgac caaagggctg ggagtgttta tgagacagca      120

tctctcagca agcaaagcaa ggcctgcaca gccccgcctt ttcctccagt gaggcgcact      180

gttcattaag gagtgttcat gagattacat tttccatcaa gcccagccag tcacgcacag      240

ctctacctct tcctctgccg ccccgcaa                                         268
```

```
<210>    83
<211>    989
<212>    DNA
<213>    Homo sapiens

<220>
<221>    unsure
<222>    position is 878 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 884 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 918 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 929 nucleotides
<223>    "n" refers to an undetermined base

<220>
<221>    unsure
<222>    position is 973 nucleotides
<223>    "n" refers to an undetermined base

<400>    83
```

```
gggtaatggg ggtgaacaga gagggatgcc gaggccagct tgtagtgtgg ctgttggtct    60
tgtccatcct atggcacaac cctgtcacca cccagatttt gttaggagtc ctcccccaac   120
ttgagagtgg aagctccttt ggcacaaaaa ggggttctgc atcatccccc agcccccagc   180
cctgagcctg ggtctggctc tgaactagac ctccatgaat gaatgcacag catcagtggg   240
gatccaccat catggggaaa tagtagatac aggaatgatt ttccaaccag attacagact   300
atttcaagcc cagccagagc ctaccaggcc aacattcccc aggcttgtgc ctctccgagc   360
ctcagattgc tcatccttca aacgagggac agctctgctg gcattacctg aactctaggg   420
tcctttataa gctcagactc cagcttagag cacacattga gaggctgctg caccccagag   480
ccacatacgt gcaacagagg gtggtccaga ccccttattg gtccccatgg ggtttgagag   540
agaagcctcc agaccagctc aacttctccc tcatctcact taggcctttg cacccagctc   600
ttaggaggtt gtcaggtcac agtgccccat ttcttttctc ttccccagaa atcatgcggg   660
ggatacctgc tcagacagga ccttcatgaa agccaggctg tgaggtgtgt tggggaatgc   720
ataattgata ggccatcgtt cggaggccct cctggaggac caaaatgtaa tcagcagtgg   780
cgagcttgtt cacgacagga attcctttta catcctggtg aggccaaaga cctggcaagc   840
aagtccctct ggtcattaaa gaagcatcct gacttgangc aggncacctt aggtcactgc   900
agccacaaaa atctttgntg ctggattcna aagtaggcat tggggctggg atctgggctc   960
tggcatcctt gancgtgtcg ggggccaaa                                     989
```

```
<210>  84
<211>  250
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 37 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 40 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 49 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 75 nucleotides
<223>  "n" refers to an undetermined base

<400>  84
cgggctcgaa acttcgaaga ccgcggaacc cgaagcngcn cttggctcna atcgcttcgg   60
```

```
ctcgaggcgc ccgtncgggt cacgtgaggt gggggcgggc cgaagagggg ggctcccctc     120

ctcctgccgc agggttggcc gcaagtgcgc ttcaagaggc gcttgatgac ggttaatgtt     180

gcagcccgga agatgacttt tttctcctcc ttgggttgcg gcaggccgtt agtgggaggt     240

cgcgtcccga                                                           250
```

```
<210>  85
<211>  402
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 224 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 265 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 382 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 390 nucleotides
<223>  "n" refers to an undetermined base

<400>  85
ttctcccttg tcatcccctt accagagcca cagaaattat ccctgtgggc tcccttgtcc      60

tcactcggcc ttttctggag ttaagagatc caagccaact actgggtctg ttccctgcta     120

aaatcttagg ccggcgtccc atccacccat ccccatgcct aggacttta agctggcaac      180

ggtacctggg tttagttttc ccttcgtata tcactatctt cgtngcttac cttcttgtgc     240

ctaaagttcc accgatgtgc aaggngatta accactaaag tgcacctgac actactcttg     300

acaaattgca gttgggaggt gagttgatga ctggccggta aatcaaaagt gcttatttag     360

ggagtgaggg ggcccgcggc anaagccgan ttccagcaca ct                       402
```

```
<210>  86
<211>  595
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
```

```
<222>  position is 157 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 377 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 410 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 441 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 444 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 456 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 461 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 473 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 490 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 525 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 532 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 534 nucleotides
<223>  "n" refers to an undetermined base
```

```
<220>
<221>  unsure
<222>  position is 541 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 572 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 575 nucleotides
<223>  "n" refers to an undetermined base

<220>
<221>  unsure
<222>  position is 583 nucleotides
<223>  "n" refers to an undetermined base

<400>  86
gatcccagaa ggttctggag ccgagtatca gagtttgagc agcgagtcca gcctagcaga      60

agcgggtgtt gaccggagac ttttcaatgg tgcaaaatga cacactgctt ttgacttggg     120

gatctgtccc ttgtggcacc agaagctaca acaggtncac ctggattcca gctctagctg     180

gactcggtaa ttgctaagtg ccagctctga agtctgtgat tccgtggaaa tccctttcaa     240

gcccgaattc tgttttttat gggcctcttg tccaaacagt ttgacttgtg aactctgttt     300

ctgtcaagtt gacacttggg cttggcaccc attcatgagc cagatgaaag cggctaaatg     360

cccgaaaaaa taaaggnttt tacctttttt ttgaaccatt ggtgagcatn taaaaaaatt     420

agggaaggta aaacccaacc nggncaaacc caactnaaca nttttttttt ccnaaacaag     480

gggggggctan tttttcactt ggaaaaacaa acaattttaa ttgantcttg ananggtgga     540

naaccaaaat tttttgttgg gttgggttcc gnagnccgaa ttntgcaaat ttctt         595
```

```
<210>  87
<211>  304
<212>  DNA
<213>  Homo sapiens

<220>
<221>  unsure
<222>  position is 279 nucleotides
<223>  "n" refers to an undetermined base

<400>  87
cgtggcccga tgcattcagg gagccctctg tgttggccgc atagcaggtg tagttgccgg      60

catcctggat gaagacgggc gcgatctgta gaccccccga ttcaagaagc atgaacctag     120
```

gaatccggac agagccactg gccagaatgt ggttttctaa agaacagtgg agaaaagagg   180

catgttacag tcgtaacgct tgaaggaaat gaagatagtg gttagagcca taagcaagta   240

atatggttcg gctccgtgtc cccacccaag tctcgtctng aattgcaatc cccacgtcgg   300

cgca   304

<210> 88
<211> 296
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 9 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 31 nucleotides
<223> "n" refers to an undetermined base

<400> 88
ggctttcgnt aggagttaat ggggcattgg ngggtgggat ggcagggctg ccagcatctg   60

acccaggagg ctgggaggag gctgctgtgt gaatacacgc tcggcctctc acagtggctg   120

ccgccgcatt agccccttgt gcttcaggga acagagcatc cgtgatggat gagactttaa   180

ttaaagtaat gagacattta taatcgcggt tatctccaaa attaggcctt ttagcaatta   240

ttcctgggga atattcctcc ggtagatagc tcccttttta gaacaacgtc ggcgca   296

<210> 89
<211> 220
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 10 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 24 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 29 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 30 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 31 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 38 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 45 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 87 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 99 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 134 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 158 nucleotides
<223> "n" refers to an undetermined base

<400> 89
attggcccgn caggcgggaa acangctgnn nttctctnac cgttntccag cactgcccag   60

accaggaggc gcagggagag gaggggncag cggttccgng accgctcctc ccgctgtccc   120

tgctctccag cctntgcctc tgcaggagcc cgcgggantt gccccaggcc cctgtcccca   180

cctgtggctc ccgtcctggt cgctcccggg gccgcggcaa   220

<210> 90
<211> 273
<212> DNA
<213> Homo sapiens

<220>
<221> unsure

<222> position is 2 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 7 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 10 nucleotides
<223> "n" refers to an undetermined base

<400> 90
gnagggnggn ggtcgcggac gccggtgggc agttcttgtt cggtgatgtg ggttaaaaag   60

gactgcagcg aggagccggg gcggcgctcg gagtaatcac cggcggcatc aaaaagcgcc   120

atcatggcat cgaggtcgcg gtctgcttgg gagccggtgg cgccgccgcg caaggcagat   180

gcctgcaggc gcatatccag ctcggtagcg ctccatacct cccacaggat ttcttccaca   '240

gaggcttggg cttgtatagc ctgccgcccc gca   273

<210> 91
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 10 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 12 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 212 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 218 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 356 nucleotides
<223> "n" refers to an undetermined base

<400> 91
acggcttctn tnctaagtga cacggtgtgt gaaattcggt tggggaggta gttctgtaaa   60

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ctgcgtctcc ccgccagcta aggaagttga gtgaagggag cgttgccgtc tgggaatcgt      120

agtcctcaca aaggcgtgag taggcggcaa ataaggattt gggtttagcc ttggggattc      180

actcctgtca aagctgttag agaagctccc anaactcnta aagtaacaga aactacttgc      240

ggcaacattt gtaacttcca cctggctcat tatcttccac tgttaccttg tgttctagat      300

aagttataat ttattctaca tatcgttcag aagtcttgtg cctgttccat attgtnagca      360

t                                                                      361
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<210>   92
<211>   462
<212>   DNA
<213>   Homo sapiens

<400>   92
gctgcccaca ctggatggga aggaccggcg cctgcagcat ctgccctcca agccttcgta       60

gctccctcct tcctgcagga taaactctaa actccttagc acaacgtggg agccttctca      120

gagactgggt ccaacccatc tccagccgca gcctcccctc ctggccccac tgccacaccc      180

ccgggcctcc ggccacactg agcctctccc ggtttcccag gatacaacac tcgcccattc      240

atagtgtggt gccttttgca cgtgctgttc ctctgcttgg ggatgctgtt ggtctttctc      300

agccaggtga agaggacgct gaatgtcacc tgcttgagta tcaggaccgg ggactgggcg      360

ctggacctag actcttggcc ctggagagaa gccctgcatg gggccgcagc ctgcccccgt      420

ccctgctcac agaaaagctc agccttgcag ccgcgtggga ga                        462
```

```
<210>   93
<211>   591
<212>   DNA
<213>   Homo sapiens

<400>   93
caaagtcacc tccacggtgc ggctcagcag ctcggcacac ttggtcatgg tgtcggggaa       60

ggcgccctcc agctgtaggt gggtagtggc agaacaggag ggtgagggga gagtccgaac      120

tgtccccact tggccgttcc ctccccactg ggggccctg agccagtggc ctcctctctc      180

ggggcctccc cggaaggagc caaggtctgt ctgcgaggca ccggtccccg gccacggcca      240

tcagccccca gaggtggatc agggcatcac ccccactcca cagctgaggc caggggggtca      300

gggaggcaac cagggcagac ctggaacctg gctctgagac aggacggccg agggcccctc      360

cactctccct ccctcggggt gggcactgac ctggacgcca aagatgtcct cacactggtg      420
```

```
gcgtttgagt agggcccact cggacatctg gccctgcagc aggttggtgc agacggccat         480

ctctccacat gtcacatccg ccccgaagcg cttgcagatc cgtcggaagg gcaggttccc         540

acactgcggg gggagcagga cagacacaca tgctcttgca cgcgcacctc a                  591
```

```
<210>   94
<211>   279
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 3 nucleotides
<223>   "n" refers to an undetermined base


<400>   94
ttntgagttt tggcctgccc acagtctagc cctggacaga gaatccgagg ctcagccatg         60

ctgcagcacc caggacactg catcccagca cctgcccgaa aatcagccca gggacccaaa         120

ggaaagcagg ctccaagctc cccggaagcc aaggaaaata ggaaaacata tcctgccccg         180

gggacacctt ctggaactat gaccacatgc acttgacctt ccggaacaat caccgcatgc         240

acctgacctc ccggaactgt caccaccgcg cgcacctca                                279
```

```
<210>   95
<211>   351
<212>   DNA
<213>   Homo sapiens

<400>   95
cctttattat tgttaaacgt cacccagaaa acccttaact cttagacagc ggctctcatt         60

aagcaaaagg ggaggcacat gaagctccag gcagggccgg gagggaaccg tgaagccaaa         120

ggctctggga gcccccaggc acctgcgttt gcattttcat cctggaggag accaggcctc         180

tggggctgct ccccggggtg cagagaggag gggtctttct tggtgtgtaa catactcatt         240

gattcagtca cctgaccttt gactccatgt attttgttga gtctggatgt gtggtgtgct         300

ctgcccagca gctgggatcc acatgagcac agacatggtc ccccgcggc a                   351
```

```
<210>   96
<211>   171
<212>   DNA
<213>   Homo sapiens

<400>   96
ttgagtgtcg cgtgaatacc taggggacac tcaggggaat gatggctccc ccgagaggta         60
```

aagggtggaa agaaggggcc tcagcaggtt aggtcttgct gggtccttct gtagggcgtc   120

tgggagatag atccgtgggg ctcctagggt cgcccctacc cggcgcgggc a   171

<210> 97
<211> 743
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> position is 155 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 181 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 202 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 228 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 259 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 262 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 293 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 366 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 386 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure

```
<222>   position is 388 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 447 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 470 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 484 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 502 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 512 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 516 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 590 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 664 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 667 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 673 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 695 nucleotides
<223>   "n" refers to an undetermined base
```

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<220>
<221> unsure
<222> position is 717 nucleotides
<223> "n" refers to an undetermined base

<220>
<221> unsure
<222> position is 742 nucleotides
<223> "n" refers to an undetermined base

<400>  97
cctccctggc ccttgttccc aaggagcttc ccttgtccca gcctcttcgc cagtgacttc       60

tcactggacc attcctttac aaggagcctg ttttttgtgt tttttttta cacctttttt      120

cttctatttc acagaaggaa caccggacgt ccctntgtga tggcagcagc catgctgcct      180

ntgtttccgc tcaggggttc tntgccacct ccaattccac ccagtctntt ggcctcggct      240

gggcttcggc tcccgcctnt gngccaaaaa ttgcaatgcc cgcggtcagg gcnctttgcg      300

gagtctcacc gcctgcggag gcttgattcc ctcctcacag gcagcagcgt ttgatggccg      360

gtgacncccc cctttccaag cacatntntc atggcccctg aatgccactt acagggcgtc      420

cctccctgtg ctaagtgctg cctgganctt tgggtgtggc agcagcaaan acctctaccc      480

ttgnggatgt tcgtttcggg gnggaaagac anatancaaa gttggtcgta aactgtaaag      540

tgtgctggga ggaaactgag gcagggaggg cctggtgcca ctggggagcn ctgccccgac      600

cccatgtgct tcccaggctc ccttggagcc acgtggatgg cgacttcctg accttggagg      660

ccgnggncct cantcctcat gctcgatggc gtcancccc tcttggggaa atccaancat      720

tcctgacctg aaaatgcacc cnc                                             743
```

```
<210>   98
<211>   589
<212>   DNA
<213>   Homo sapiens

<400>   98
ttgccgcgct gataaaggaa gcgtctagaa ggtctcccca gccttcatca tctgagactt       60

ggctttcagc cccaaagcac taggccctgc tgttaacctt ccaccattaa cctttggtgc      120

tcttcaatta gcagcagcca ggggtccttg gcaggtatga gaatttggaa ggacagcccc      180

agggcatggc ccccggctgc agcaaaagtt ctaagtgttc ttctgttgga aggaagccca      240

ggagatattg atcagctgca ggtgggggag gccccagatc ccacccttgc ctgcctccag      300

gagaaggttc tccatgggcc aaaatggagg cagagtccca ctttgcctgg gcagctccct      360
```

```
gagcatggct ccctgtggac ggagctgagt gacgtcatga ctctaggcct caacaaaaga      420

gctttggaaa atcccgatga ttcgaattgt attaaatcaa caaacatcgg gttgcacagt      480

tactagaaaa cggagatctg cgtcatcact tactagacac gtgaccttga acggcggctt      540

ccccgtgtga aacagcaaag ttctgtaacc cccatgaacg cgcctctca                  589
```

```
<210>   99
<211>   538
<212>   DNA
<213>   Homo sapiens
```

```
<400>   99
tgccgcgtct gaccctactc tcacaaagac tttccaacta gcataattga gttaaatggt       60

cccccaact cccttaattc aagctaaact tgcagtttaa caactatagg agtgatatct       120

acacattaat gccacacttt aacatgccta acactacaca tgaacacgct tccgggtgct      180

gttacatccc gctctctccc aagcacgaga cacaggcagg atgctgacgt cctgcttctc      240

tgctgcgggc gggaagtcaa gactccggat ttgctgcagg agttgccgtg gggatcctga      300

cttcacgcag gagatggtcg gcctctggaa gtgcctggcc cgtttatcct tgaaatctac      360

ctgtgcaggt ggtccttgcc tcagcccctc aggacaacac aggtctttcc taagttacag      420

ggagaccatc agattgtcgt gtccgagccc cctgaagtgg aacccacagt ctccattcag      480

tctgccctca gtttccctcc cctctgcagg gccattgctg ctgtggacgc gcctctca       538
```

```
<210>   100
<211>   486
<212>   DNA
<213>   Homo sapiens
```

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<400>   100
agaggtagaa aaaggagtta gaagcaaaga ggaaaaaata aataaacagg caacaaaaac       60

ccaacccagc cagcctgagc catttgcatt agtgttcatt taggaaatta gcagacggga      120

aacgctgggg agtggagtgg gccccggcct tggggactgc agagcccgct cagccctggg      180

tggctgggcc cacatgggct gtgccccagg agcacaggag gacccagagg gtggccgaga      240

gagcctcgcc gggctccggt atgggtcctg gcccctcaca ggtgcgagcc tggcccagtg      300

actgtggacg ctgtgggaga gcaggcctcc gatacgcagg gctgggactg ctgacctgga      360

aggtggtgcc gggcgtgtct ggtgaaggcg ccgttggcag ctagagagag acggcggatg      420

gggtgacgcc attacccacg gtcccagttt tgaggcttga cggtgacgga aaaggacgtc      480

ggcgca                                                                486
```

```
<210>   101
<211>   450
<212>   DNA
<213>   Homo sapiens

<400>   101
aattgaacca gggtgcacgg ccagcgccag acacagtgag cttcatggca actccagttt      60

accggtgaga accatggggc cactcagaga ggcaaagagc ctcacccgag tgagtcctct     120

ggcttctccc cacctgggcc gggccccagg ccgcgctgtg gttccctttc cagccgtcat     180

ccctgggtga tgggaggtgg gcattctgtt caaccttgtg ggtcagggag ccagggccag     240

tgtgcagatg agaagaggct gcggttactg gcgatgcgag ggactgtccc cttcgtgggc     300

actttctctt ttgaggccag tgaaatgtgt tccctggggt tgtattcctg agaaggcctc     360

atttaaaggg agccgccaaa ccaagtgggc ttagcaaaag cagtttgtca cctggcagca     420

cgtgtgagcc tcgcccggac gcgcctctca                                      450


<210>   102
<211>   292
<212>   DNA
<213>   Homo sapiens

<400>   102
agcgcggcct ggcagattgc ccattaatga aactcagtgg gcagaggctg ctgagggaca      60

cggattccca ctccccgggg gaggggtgg aaatggcttc ctccctctgc ttccctacca     120

ccagtaatgg ggagctcacc atgcttagaa gactcttcct tgcatggagt tcgggcctcc     180

tccctgcacc taccacccta gtggccccaa gtcttaaggc tgaaggttaa tcctgtgtcc     240

ttcagaagca aaggctgcaa ccgataccaa acagaggtgg ccagcgcggg ca            292


<210>   103
<211>   395
<212>   DNA
<213>   Homo sapiens

<220>
<221>   unsure
<222>   position is 340 nucleotides
<223>   "n" refers to an undetermined base

<220>
<221>   unsure
<222>   position is 367 nucleotides
<223>   "n" refers to an undetermined base
```

<400> 103

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agagcttatc ccgcgagcac aagggagccg gggcctgggc cgccgtggga aggggctcct      60

gccttccggg gacgcggtca gggaagtcca gccggggtgc tctctgcact gcgggtgccg     120

ggctcggcag aggccaaccc ggcaaaacga gcaggatctc ccggccccac cctagtgggc     180

tccgcctgcc ccaacaacca tcctgccatc ctccctgcga gacaggtgac tttcctctct     240

gatgcggtgc atctgtcatc tgtctaacgg gcccattccc cagtgaaaca cccccaacca     300

aagacacgaa ggggaaggcg caagcttcta ccaagctcan tttgcccatc tggtgcccac     360

ctgcctngta tttggtgact tggaggatag gaagg                                395
```